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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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and is derived by analysis of the total score distribution. Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

Protein encoded by	AAW14741	18	540	10.1	69	11
Protein encoded by	AAW14740	18	476	10.1	69	TO
Potato class B sta	AAW69300	19	906	10.2	70	
Potato starch bran	AAW71290	19	906	10.2	70	. &
Pseudomonas stutze	AAE05866	22	513	10.7	73	7
Human TCL-1 polype	AAR94975	17	113	19.3	132	6
Human polypeptide	AAM4 1609	22	129	21.8	149	·
Human polypeptide	AAM39823	22	114	21.8	149	4.
Human TCL-1 polype	AAR94974	17	113	21.8	149	. (4)
Mature T-cell prol	AAR94976	17	108	25.8	176.5	. 2
Amino acid sequenc	AAB18763	21	128	100.0	685	
Description	Ħ	BB	Match Length DB	Match	Score	No.
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S	SUMMARIES					

16 AAR85439 18 AAW14737 7 AAP61316 11 AAW85028 12 AAR15054 13 AAR75053 14 AAY70531 15 AAW54377 21 AAY94880 22 AAB94032 20 AAW97993 22 AAB94032 20 AAW97995 22 AAB94032 24 AAR41424 25 AAR41424 26 AAR41424 27 AAR41424 28 AAR41424 29 AAR41424 21 AAR41424 22 AAB94031 24 AAR41424 25 AAB95043 26 AAR97995 27 AAB95043 28 AAR640314 29 AAR640314 21 AAG40314 21 AAG40314 21 AAG40314 21 AAG40313 21 AAG40313 21 AAG40313 21 AAG40313 21 AAG40314	Amino acid sequenc Arabidopsis thalia Arabidopsis thalia		21	1012 762 764		65.5 65.5	4 4 4 3 I
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	SIS	AAR8543	16	1012	10.1		12

## ALIGNMENTS

ri Cioce (m, Pekarsky r; XX	XX	PA (UYJE-) UNIV JEFFERSON THOMAS.	PR 15-MAR-1999; 99US-0124714.	PF 15-MAR-2000; 2000WO-US06612.	XX	PD 21-SEP-2000.	XX	PN WO200055169-A1.	OS Homo sapiens.		T-cell leukaemia;	Tcl-1; Tc1-1b; T c		Amino acid sequence of the human		DT 22-JAN-2001 (first entry)	AC AAB18763;	AAB18763 standard; Protein; 128	AABIU/63
		THOMAS.	24714.	06612.						,	immunodeficiency syndrome;	maliqnancy; chromosome	,	the human Tcl-1b prote	,	try)			

ataxia-teleangiectasia. 14 abnormality; lymphoma;

PT PT XX Novel nucleic acid of Tcl-1 gene family, Tcl-1b, expressed in low levels in normal bone marrow and peripheral lymphocytes, but activated in T-cell leukaemia and lymphoma, used to identify chromosome 14 abnormalities

WPI; 2000-611514/58. N-PSDB; AAA75822.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a human Tc1-1b protein. The Tc1-1b gene is implicated in the development of T cell malignancies. Fragments of Tc1-1b cDNA sequences are used for detecting a target sequence indicating a chromosome 14 abnormality, such as a (14:14)(q11:q32) translocation or a (14)(q11:q32) inversion. Tc1-1b antisense sequences and antibodies are useful for treating a disease state such as T-cell leukaemia or lymphoma associated with a chromosome 14 abnormality. The Tc1-1b gene and its gene product are useful for treating disease states associated with the Tc1-1b locus on chromosome protein including T-prolymphocytic leukaemias, acute and chronic leukaemias associated with the immunodeficiency syndrome ataxia-teleangiectasia (AT).
         New TCL-1 protein and gene associated with chromosome 14 abnormalities - useful to develop prods. for detection, transportation of diseases such as T-cell leukaemia(s) and prevention of diseases such as T-cell leukaemia(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 64; 70pp; English.
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mature T-cell proliferative 1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR94976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                   WPI; 1996-239444/24.
                                                                                                                     Croce CM,
                                                                                                                                                     (RAGG-) RAGGIO-ITALGENE SPA. (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                       27-OCT-1994;
                                                                                                                                                                                                                                        23-OCT-1995;
                                                                                                                                                                                                                                                                          09-MAY-1996.
                                                                                                                                                                                                                                                                                                           WO9613514-A1
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                              T-cell proliferative 1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCL-1; chromosome-14; leukaemia; lymphoma; therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR94976 standard; Protein; 108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 tyqperkd 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TYQPERKD 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 vhlwqmavhtrellssgqmpfsqlpavwqlypgrkyraadssfweiadhgqldsmeqlv1 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 VHLWQMAVHTRELLSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSMEQLVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 100.0%; Score 685; DB 2 Local Similarity 100.0%; Pred. No. 1e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MASEASVRLGVPPGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWARASQGSRYEPSIT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 maseasvrlgvppgrlw1qrpg1yedeegrtwvtvvvrfnpsrrewarasqgsryepsit 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 AA;
                                                                                                                     Russo G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                       94US-0330272.
                                                                                                                                                                                                                                        95WO-US13663.
                                                                                                                                                                                                                                                                                                                                             /note= "unidentified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21; Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                   treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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RESULT
AAR94974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
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   CCC XX PT PT CCC CCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome 14 abnormalities leading to leukaemia and lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The mature T-cell proliferative 1 protein (AAR94976) is involved in a translocation of chromosome 14 and X chromosome t(14:X)(q11:q28). It shows 40% amino acid sequence homology to human TCL-1 protein (AAR94974), which is associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 69; 105pp; English.
The amino acid sequence of human TCL-1 protein (AAR94974) was deduced from a cDNA clone (AAT18876) obtd. from an ALL1 cell line cDNA
                                                       Claim 6; Page 68; 105pp; English
                                                                                                          New TCL-1 protein and gene associated with chromosome 14 abnormalities - useful to develop prods. for detection, tr and prevention of diseases such as T-cell leukaemia(s) and
                                                                                                                                                                                    WPI; 1996-239444/24.
N-PSDB; AAT18876.
                                                                                                                                                                                                                                                                                                                                  27-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCL-1; chromosome-14; leukaemia; lymphoma; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human TCL-1 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR94974;
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                                                                                                                                                                                                                                         Croce CM,
                                                                                                                                                                                                                                                                                                                                                                                                     09-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9613514-A1
                                                                                                                                                                                                                                                                           (RAGG-) RAGGIO-ITALGENE SPA.
                                                                                                                                                                                                                                                                                                                                                                      23-OCT-1995;
                                                                                          Lympnoma(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 LVLTYQPE 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 SITVHLWQMAVHTRELLSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSMEQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 25.8%; Score 176.5; DB 1 Local Similarity 33.6%; Pred. No. 4.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 mage---dvgappdh1wvhqegiyrdeyqrtwvavveeetsflrarvqqiqvplgdaarp 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MASEASVRLGVPPGRLWIQRPGIYEDEEGRTWVTVV---VRFNPSRREWARASQGSRYEP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
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                                                                                                                                                                                                                                         Russo G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                  94US-0330272
                                                                                                                                                                                                                                                                                                                                                                        95WO-US13663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Phosphorylation_site
/note= "casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Mismatches
                                                                                                                                  for detection, treatment
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                                          Tang YT,
                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                09-JUL-2000;
                                                                                                                                                                                                                                                                                           21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                           peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral Sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                    29-NOV-2000;
                                                                                                                                                                                                                                           03-AUG-2000;
                                                                                                                                                                                                                                                                                                                    26-DEC-2000; 2000WO-US34263.
                                                                                                                                                                                                                                                                                                                                              26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            library. Recombinant TCL-1 can be obtd. by incorporation of the cDNA into a vector and expression in Escherichia coli transformants. The TCL-1 protein and antibodies raised against it can be used for the diagnosis and treatment of conditions associated with increased expression of TCL-1 proteins and/or with chromosomal abnormalities, esp. T-cell leukaemia and lymphomas with chromosome 14 abnormalities.
                                                                                                                                                                                                                                                                                                                                                                                                                                chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human polypeptide SEQ ID NO 2968.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM39823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM39823 standard; Protein; 114 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                           Leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 PGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWARASQGSRYEPSITVHLWQMAVHTRE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 pmtptqigpsllpimwqlypdgryrssdssfwrlvyhikidgvedmllellpd 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 pdrlwawekfvyldekqhawlpltieikdrlq------lrvllrredvvlgr 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 LLSSGOMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSMEQLVLTYQPE 125
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                                                                                    2001-442253/47.
DB; AAI58979.
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33;
                                                                                                                                       Wang Z,
                                                                                                                                                 Liu C,
                                                                                                                         Zhou p,
                                                                                                                                                                                                             2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
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                                                                                                                                                                                                     2000US-0727344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                      Wehrman
                                                                                                                      Asundi V, Chen R, Ma Y, Qian XB, Wehrman T, Xu C, Xue AJ, Yang Y, Goodrich R, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
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Pred. No. 7.6e-10;
21; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 113;
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                                                                                                                                              Ren F,
                                                                                                                                 Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                                           Wang D;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and

WPI; 2001-442253/47

Example 4; SEQ ID NO 2968; 10078pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance, peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
                               Zhao QA,
                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as localised neuropathies and central nervous system disease, such as lateral sclerosis, and Shy-Drager Syndrome. Other uses include the lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                              Tang YT,
                                                                                                                                                                                                              09-JUL-2000;
                                                                                                                                                                                                                                                                            26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                               26-JUL-2001
                                                                                                                                                                                                                                                                                                                                               W0200153312-A1
                                                                                                                               29-NOV-2000;
                                                                                                                                                                               03-AUG-2000;
                                                                                                                                                                                                                                               21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human polypeptide SEQ ID NO 6540.
                                                                                                                                                                L4-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                               leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM41609;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \text{C.N.}\,\text{S} disorders. Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 pmtptqigpsllpimwqlypdgryrssdssfwrlvyhikidgvedmllellpd 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 LLSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSMEQLVLTYQPE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 PGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWARASQGSRYEPSITVHLWQMAVHTRE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 pdrlwawekfvyldekqhawlpltieikdrlq--
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                         Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 AA;
                                                                                                                                                       2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
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                                                                                                                             2000US-0693036
2000US-0727344
                         Asundi V, Ch
Wehrman T, X
Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.8%;
                                        Chen R, Ma Y, Xu C, Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 149; DB 22;
Pred. No. 7.7e-10;
                           Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
                                                      Qian XB,
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                                        Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 114;
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                                      Zhang J;
                                                          Ren F,
                                                    Wang
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RESULT
AAR94975
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as a localised neuropathies and central nervous system diseases, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are uniqueness of the contract of the contrac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAI60765.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; SEQ ID NO 6540; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       /note= "unidentified amino acid" Wisc-difference 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification.
                                                                                                                                                                                                                                                                                                                                                         Misc-difference 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers Misc difference 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human TCL-1 polypeptide.
(RAGG-) RAGGIO-ITALGENE SPA
                                                                   27-OCT-1994;
                                                                                                                                23-OCT-1995;
                                                                                                                                                                                                09-MAY-1996.
                                                                                                                                                                                                                                                            W09613514-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCL-1; chromosome-14; leukaemia; lymphoma; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR94975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR94975 standard; Protein; 113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 pmtptqigpsllpimwqlypdgryrssdssfwrlvyhikidgvedmllellpd 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 pdrlwawekfvyldekqhawlpltieikdrlq------lrvllrredvvlgr 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 LLSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSMEQLVLTYQPE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 PGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWARASQGSRYEPSITVHLWQMAVHTRE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                94US-0330272
                                                                                                                                95WO-US13663
                                                                                                                                                                                                                                                                                                                             /note= "unidentified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "unidentified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                             'note= "unidentified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.8%; Score 149; DB 22; Length 129; 29.2%; Pred. No. 9.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 14; Gaps
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                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The amino acid sequence (AAR94975) of human TCL-1 protein was deduced from the exon sequences of the TCL-1 gene (AAR98877). A sequence deduced from a cDNA clone is given in AAR94974. The TCL-1 gene is expressed at high levels in leukaemic cells carrying a t(14:14)(q11;q32) translocation or an inv(14)(q11;q32) inversion. The TCL-1 protein, and antibodies raised against it, can be used for the diagnosis or treatment of conditions associated with increased expression of TCL-1 proteins and/or with chromosome 14 abnormalities, esp. T-cell leukaemia and lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New TCL-1 protein and gene associated with chromosome 14 abnormalities - useful to develop prods. for detection, treand prevention of diseases such as T-cell leukaemia(s) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAT18877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Croce CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 69-72; 105pp; English.
                                                                                                                                                                                                                                                                                Open reading frame-O; ORF-O; pyridine-2,6-bis (thiocarboxylate); PDTC; environmental remediation; phytoremediation; bioaccumulation; water purification; solution mining mobilisation; immobilisation; detoxification; redox state modifier; metal ion reactivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE05866 standard; Protein; 513 AA
                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas stutzeri open reading frame-0 (ORF-O) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                    24-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE05866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lymphoma(s)
                                                                                                                                                                                                                                                                   carbon tetrachloride; metal
                                                                                                                                                                                     WO200153309-Al.
                                                                                                                                                                                                                        Pseudomonas stutzeri.
                 (IDAH-) IDAHO RES FOUND INC
                                                          20-JAN-2000; 2000US-0177251
                                                                                                19-JAN-2001; 2001WO-US02386
                                                                                                                                            26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 lpd 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 QPE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 pdrlwawekfvyldekqxacipltieikdrlqxxvllrredvvlgrpmtptxigpsl--- 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 PGRLWIQRPGIYEDEEGRTWVTVVVRFNPS------RRE---WARASQGSRYEPSITVH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 LWQMAVHTRELLSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSMEQLVLTY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 19.3%; Score 132; DB 17; Local Similarity 26.8%; Pred. No. 7.6e-08; es 33; Conservative 17; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1996-239444/24.
PASZCZYNSKI A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Russo G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----lpimwqlypdgryrssdssfwrlvyhikidgvedmllel 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 34; Gaps
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AAW71290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
Modifying starch producing organisms, particularly plants - by expression of nucleotide sequences which code for introns of starch % \left( 1\right) =\left\{ 1\right\} 
                                                           WPI; 1998-480801/41.
N-PSDB; AAV54979.
                                                                                                                  Poulsen P;
                                                                                                                                                 (DANI-) DANISCO AS.
                                                                                                                                                                                   24-MAR-1997;
21-FEB-1997;
                                                                                                                                                                                                                                                                                                           W09837214-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ORF-O) protein. The Pseudomonas stutzeri genome includes ORFs that encode enzymes required for blosynthesis of pyridine-2,6-bis (thiocarboxylate) (PDTC). The ORFs encoding PDTC are especially useful in environmental remediation methods, e.g. phytoremediation, bioaccumulation, water purification, waste water purification, solution mining mobilisation, immobilisation, detoxification, redox state modifier or modification of metal ion reactivity. In particular, the ORFs are useful for degrading carbon tetrachloride and removing metals from substrates, e.g. soil or water.
                                                                                                                                                                                                                                                                                                                                            Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                        Potato; starch branching enzyme; SBE; class A; class B; modified starch;
                                                                                                                                                                                                                                                                                                                                                                                                                              Potato starch branching enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW71290 standard; Protein; 906 AA.
                                                                                                                                                                                                                                       23-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                              gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW71290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reducing the amount of metal or carbon tetrachloride in a substrate, e.g. soil or water
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a Pseudomonas stutzeri open reading frame-O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 164-166; 172pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acids, useful for producing enzymes required to produce pyridine 2,6-bis (thiocarboxylate), especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AADII187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-465361/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 lgqlpprwqldpsgrlsrlagtpeandmidfslpnevqmlvst 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Paszczynski A, Sebat JL, Lewis TA, Crawford RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 FSQLPAVWQLYP-GRKYRAADS-SFWETADHGQIDSMEQLVLT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 fgprtsrwsrsgkagrlrvhchhpqratcarrnrrqvfvschlrhllhhphkrrrargvp 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 FNPSRREWARASQGSR-----YEPS-----ITVHLWQMAVHTRELLSSGQMP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        513 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                 97GB-0003672.
                                                                                                                                                                                                    97GB-0006075
                                                                                                                                                                                                                                       98WO-IB00295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.7%; Score 73; DB 22; Length 513; 24.3%; Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cortese MS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a potato starch branching enzyme (SBE).

C The specification describes a method for affecting enzymatic activity in C a plant. The method comprises expressing in the plant a nucleotide Sequence encoding, partially or completely, an intron of a class A potato C SBE in a sense orientation, optionally together with a nucleotide Sequence which codes, partially or completely, for an intron of a class B C SEE in a sense orientation, optionally together with a nucleotide SBE in a sense or antisense or interation, and where the nucleotide C sequence does not contain a sequence that is sense to an exon sequence C normally associated with the intron. The method can be used for providing C genetically modified plants which are capable of producing modified and C improved starches whose properties would satisfy various industrial C requirements. They can be used for preparing tailor-made starches in C plants which could replace the post-harvest modified starches. They can C also be used for expressing genes of interest, e.g. pharmaceutically c active proteins or enzymes or proteins which are beneficial to plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Affecting enzymatic activity using antisense intron inhibition especially of starch branching enzyme in plants, useful to alter
                                                                              N-PSDB; AAV55069
                                                                                                                                                  Poulsen P;
                                                                                                                                                                                                                                                                                                                                                            27-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Solanum tuberosum cv. Desiree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Starch branching enzyme; SBE; potato; antisense; amylopectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potato class B starch branching enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-DEC-1998 (first entry)
                                                                                                  WPI; 1998-467573/40
                                                                                                                                                                                               (DANI-) DANISCO AS.
                                                                                                                                                                                                                                                                   24-MAR-1997;
                                                                                                                                                                                                                                                                                                              23-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                      W09837213-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW69300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW69300 standard; Protein; 906 AA.
                                                                                                                                                                                                                                             21-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     branching enzyme sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        668 sflasgkqivssmdddnkvvvfergdlvfvfnfhpkntyegykvgcdlpgkyrvaldsda 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 8; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      621 widfp----regnnw----sydkcrrqwnladsehlryk---fmnafdramnsldekf 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             728 wefgghgr 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 WEIADHGQ 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 WIQRPGIYEDEEGRTWVTVVVRFNPSRREWARA-SQGSRYEPSITVHLWQMAVHTRE--- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 -LLSSGQMPFS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31; Conservative 17; Mismatches 34; Indels 46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            906 AA;
                                                                                                                                                                                                                                        97GB-0006060.
97GB-0003663.
                                                                                                                                                                                                                                                                                                              98WO-IB00270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.2%; Score 70; DB 24.2%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----QLPAVWQLYPGR-------KYRAA-DSSF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 19; Length 906;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC enzyme (SBE) of potato Cv. Desiree. It was deduced from a CC full-length SBE gene sequence (see AAV5509). A novel method of affecting enzymatic activity in plants or other starch-producing corpanisms (or their cells, tissues or organs) comprises expressing CC anucleotide sequence coding for an intron (see AAV55046) of a class CC A potato SBE in an antisense orientation, but not containing a CC sequence antisense to an exon sequence normally associated with the CC intron. The sequence is optionally expressed with a nucleotide CC intron. The sequence is optionally expressed with a nucleotide CC ensemble codes, partially or completely, for an intron of a CC class B SBE in an antisense/sense orientation. Also claimed are a CC promoter (see AAV55047) useful in expressing the nucleotide sequence CC of the method, a transgenic starch-producing organism, and the CC production of transgenic starch-producing organisms with altered CC production of transgenic starch-producing organisms with altered CC camylopectin levels and/or starch composition.
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           starch branching enzyme activity, amylopectin levels or starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the amino acid sequence of the class B starch branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Fig 12; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                 Snyder D, Vakharia V;
                                                  (UYMA-) UNIV MARYLAND BALTIMORE
                                                                                                       23-MAR-1994;
04-MAY-1990;
                                                                                                                                                             04-MAY-1990;
                                                                                                                                                                                               21-JAN-1997
                                                                                                                                                                                                                                    US5595912-A
                                                                                                                                                                                                                                                                     Infectious bursal disease virus
                                                                                                                                                                                                                                                                                                        Gumboro disease.
                                                                                                                                                                                                                                                                                                                           structural
                                                                                                                                                                                                                                                                                                                                                                              Protein encoded by IBDV clone GLS-3.
                                                                                                                                                                                                                                                                                                                                                                                                               12-MAY-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW14740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW14740 standard; Protein; 476 AA.
                                                                                       28-JUN-1993;
                                                                                                                                                                                                                                                                                                                                         Infectious bursal disease virus; IBDV; large segment; GLS 5 strain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         668 sflasgkqivssmdddnkvvvfergdlvfvfnfhpkntyegykvgcdlpgkyrvaldsda 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  621 widfp----regnnw----sydkcrrqwnladsehlryk---fmnafdramnsldekf 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         728 wefgghgr 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 WEIADHGQ 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 WIQRPGIYEDEEGRTWVTVVVRFNPSRREWARA-SQGSRYEPSITVHLWQMAVHTRE--- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 -LLSSGQMPFS------QLPAVWQLYPGR------KYRAA-DSSF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 10.2%; Score 70; DB 19; Length 906; Similarity 24.2%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 906 AA;
                                                                                                                                                                                                                                                                                                                         protein; VP2; VP3; VP4; immunogen; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                     94US-0216276.
90US-0519202.
93US-0083784.
                                                                                                                                                             90US-0519202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46;
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                                                                                                                                                                                                                                                                                                                                     RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequences given in AAW14738-41 are encoded by fragments of the infectious bursal disease virus (IBDV) large segment from the GLS 5 strain. These sequences are encoded by clones GLS-1 to GLS-4. Proteir such as these, derived from IBDV, esp. VP2 which is the major host protective immunogen of IBDV, may be used to prepare vaccines against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Infectious bursal disease virus nucleic acids - for prodn. of vaccines for poultry for protection against {\tt Gumboro\ disease}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT63068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-107584/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAY-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW14741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Column 71-76; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein encoded by IBDV clone GLS-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW14741 standard; Protein; 540 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBDV infection/Gumboro disease.
                                                                                                                                                                                                                                                      23-MAR-1994;
04-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                 US5595912-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Infectious bursal disease virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gumboro disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Infectious bursal disease virus; IBDV; large segment; GLS 5 strain;
structural protein; VP2; VP3; VP4; immunogen; vaccine;
Claim 2; Column 65-70; 41pp; English.
                                    Infectious bursal disease virus nucleic acids - for prodn. Of vaccines for poultry for protection against Gumboro disease
                                                                                                                                                     Snyder D, Vakharia V;
                                                                                                                                                                                              (UYMA-) UNIV MARYLAND BALTIMORE
                                                                                                                                                                                                                                                                                                                    04-MAY-1990;
                                                                                              N-PSDB; AAT63069
                                                                                                                   WPI; 1997-107584/10.
                                                                                                                                                                                                                                    28-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                        21-JAN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266 anfals 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 EQLVLT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 ----hlamaasefketpelesavrameaaasvdpl-----fqsalsvfmwleengivtdm 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 rlg----lklagpgafdvntgpnwatfikrfphnprdwdrlpylnlpylppnagrqy-- 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 SITVHLWQMAVHTREL--LSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSM 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 RLGVPPGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWAR------ASQGSRYEP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         476 AA;
                                                                                                                                                                                                                                                            94US-0216276
90US-0519202
                                                                                                                                                                                                                                       93US-0083784.
                                                                                                                                                                                                                                                                                                                    90US-0519202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.1%; Score 69; DB 18; Length 476; 23.8%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50; Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteins
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RESULT 12
AAR85439
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                                    A cDNA clone contg. the entire coding region of the large RNA segment of infectious bursal disease virus serotype I strain GLS has the sequence given in AAT05623, and encodes the structural proteins VP224/3 (AAR85439). Chimeric immunogens in which an epitopic determinant of a lethal IBDV strain is inserted into the GLS VP2 can be expressed in recombinant mammalian and poultry
                                                                                                                                                                                        Chimeric infectious bursal disease virus polypeptide immunogens comprising VP2 with modified epitopic amino acid sequence for preparation of vaccines for immunisation of poultry
                                                                                                                                                            Disclosure; Fig 5A-K; 77pp; English.
                                                                                                                                                                                                                                                               WPI; 1995-351197/45.
N-PSDB; AAT05623.
                                 host cells.
                                                                                                                                                                                                                                                                                                                                              (UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                                                                                                                                                                             Mengel-Whersat SA, Snyder DB,
                                                                                                                                                                                                                                                                                                                                                                                   29-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-OCT-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09526196-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Infectious bursal disease virus of chickens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBDV GLS structural protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-FEB-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBDV; immunogen; vaccine; poultry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR85439 standard; Protein; 1012 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequences given in AANI4738-41 are encoded by fragments of the infectious bursal disease virus (IBDV) large segment from the GLS 5 strain. These sequences are encoded by clones GLS-1 to GLS-4. Protein such as these, derived from IBDV, esp. VP2 which is the major host protective immunogen of IBDV, may be used to prepare vaccines against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR85439;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         507 anfals 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 EQLVLT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              456 ----hlamaasefketpelesavrameaaasvdpl-----fqsalsvfmwleengivtdm 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               403 rlg----lklagpgafdvntgpnwatfikrfphnprdwdrlpylnlpylppnagrgy-- 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BDV infection/Gumboro disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 SITVHLWQMAVHTREL--LSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSM 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 RIGVPPGRIMIQRPGIYEDEEGRTWVTVVVRFNPSRREWAR------ASQGSRYEP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               540 AA;
                                                                                                                                                                                                                                                                                                                                                                                94US-0219262.
                                                                                                                                                                                                                                                                                                                                                                                                                 95WO-US03772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.1%; Score 69; DB 18; Length 540; 23.8%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18; Mismatches
                                                                                                                                                                                                                                                                                                            Vakharia V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50; Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                          This sequence is encoded by a fragment of the infectious bursal disease virus (IBDV) large segment from the GLS 5 strain. This sequence represents the structural proteins VP2, VP3 and VP4. These proteins esp. VP2 which is the major host protective immunogen of IBDV, may be used to prepare vaccines against IBDV infection/Gumboro disease.
Sequence
                                                                                                                                                      Claim 1; Column 43-52; 41pp; English.
                                                                                                                                                                                        Infectious bursal disease virus nucleic acids - for prodn. of vaccines for poultry for protection against Gumboro disease
                                                                                                                                                                                                                                                                                                                            Snyder D,
                                                                                                                                                                                                                                                                N-PSDB; AAT63065.
                                                                                                                                                                                                                                                                                    WPI; 1997-107584/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-1994;
04-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Infectious bursal disease virus; IBDV; large segment; GLS 5 strain; structural protein; VP2; VP3; VP4; immunogen; vaccine;
                                                                                                                                                                                                                                                                                                                                                                (UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                                                                                                                                                                                                                                                                               28-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5595912-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Infectious bursal disease virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gumboro disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBDV strain GLS large segment derived protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAY-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW14737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW14737 standard; Protein; 1012 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 802 anfals 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     751 ----hlamaasefketpelesavrameaaasvdpl-----fqsalsvfmwleengivtdm 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 698 rlg----lklagpgafdvntgpnwatfikrfphnprdwdrlpylnlpylppnagrqy-- 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 EQLVLT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 SITVHLWQMAVHTREL--LSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSM 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 RLGVPPGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWAR------ASQGSRYEP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30;
1012 AA;
                                                                                                                                                                                                                                                                                                                            Vakharia V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         94US-0216276.
90US-0519202.
93US-0083784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90US-0519202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.1%; Score 69; DB 23.8%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Mismatches 50; Indels 28; Gaps
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                                      698 rlg-----lklagpgafdvntgpnwatfikrfphnprdwdrlpylnlpylppnagrqy-- 750
58 SITVHLWQMAVHTREL--LSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSM 115
                                                                                  8 RLGVPPGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWAR-----ASQGSRYEP 57
                                                                                                                                                           Local Similarity
                                                                                                                                        30;
                                                                                                                                      Conservative
                                                                                                                                                  10.1%; score 69; DB 18; Length 1012; 23.8%; Pred. No. 36;
                                                                                                                               18; Mismatches
                                                                                                                               50; Indels
                                                                                                                           28; Gaps
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Sequence

1012 AA;

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RESULT 14
AAP61316
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AAR15054
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                              RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                         The avian IBDV 32kD structural protein product may be used in serological diagnosis and development of a vaccine against the disease. The protein is encoded by the only extensive reading frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant DNA corresp. to infectious bursal disease virus-RNA used for producing polypeptide(s) for use in treatment of infectious bursal disease virus in chickens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-DEC-1986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO8607060-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Avian infectious bursal disease virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBDV; poultry; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Infectious bursal disease virus 32kD structural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-OCT-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10; Fig 10; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAN60874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-AUG-1985;
30-MAY-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-1986;
 AAR15054 standard; Protein; 1023 AA.
                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                             of the sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CSIR ) COMMONWEALTH SCIENT ORG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1986-332075/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 EQLVLT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          751 ----hlamaasefketpelesavrameaaasvdpl-----fqsalsvfmwleengivtdm 801
                                                                           811 anfals 816
                                                                                                                                                                                                 707 rlg-----lklagpgafdintgpnwatfikrfphnprdwdrlpylnlpylppsagrgy-- 759
                                                                                                         116 EQLVLT 121
                                                                                                                                        760 ----hlamaasefketpelesavrameaaadvdpl-----fqsalsvfmwleengivtdm 810
                                                                                                                                                                       58 SITVHLWQMAVHTREL--LSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSM 115
                                                                                                                                                                                                                                                            / Match 10.1%; Score 69; DB 7; Length 1021;
Local Similarity 24.6%; Pred. No. 37;
les 31; Conservative 16; Mismatches 51; Indels 28; Gaps
                                                                                                                                                                                                                                     8 RLGVPPGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWAR-----ASQGSRYEP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hudson PJ,
                                                                                                                                                                                                                                                                                                                                                1021 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fahey KJ;
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Best Local S
                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR15054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Infectious bursal disease virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Infectious bursal disease virus; IBDV; vaccine; poultry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptide encoded GLS clones 1 to 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-FEB-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example; Page 30; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Infectious bursal disease virus nucleic acids – useful as vaccines against IBDV in poultry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ14897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vakharia V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYMA-) UNIV MARYLAND COL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAY-1990;
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                                                                        762 ----hlamaasefketpelesavrameaaasvdpl----fqsalsvfmwleengivtdm 812
                                                                                                                                                        709 rlg-----lklagpgafdvntgpnwatfikrfphnprdwdrlpylnlpylppnagrgy-- 761
813 anfals 818
                                     116 EQLVLT 121
                                                                                                                58 SITVHLWQMAVHTREL--LSSGQMPFSQLPAVWQLYPGRKYRAADSSFWETADHGQIDSM 115
                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                8 RLGVPPGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWAR------ASQGSRYEP 57
                                                                                                                                                                                                                                         30;
                                                                                                                                                                                                                                                                                                                                               1023 AA;
                                                                                                                                                                                                                                         Conservative
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/note= "GLS-3 clone"
999..2620
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/note= "GLS-2 clone"
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                                                                                                                                                                                                                                                             10.1%; Score 69; DB 12; Length 1023; 23.8%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .1252
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Search completed: November 29, 2001, 04:03:10 Job time: 516 sec

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Post-processing: Minimum Match 0% Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176.5
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195.814 Million cell updates/sec
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US-08-219-262B-8

US-08-708-262B-8

US-08-708-562B-8

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US-08-216-276A-19
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US-08-708-541A-34
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US-08-219-262B-9
US-08-219-262B-12
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                                                                                                               Matches
                                                                                                                                                            Query Match
1 MAGE----DVGAPPDHLWVHQEGIYRDEYQRTWVAVVEEETSFLRARVQQIQVPLGDAARP 57
                                               1 MASEASVRLGVPPGRLWIQRPGIYEDEEGRTWVTVV---VRFNPSRREWARASQGSRYEP 57
                                                                                                                                    Local Similarity
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Database :

Sequence:

Title:

Run on:

Result

8 9 10 11 12 13 13 14 15 15 16 17 17 17 18 19 20 21 22 23 24 27

Conservative 17; Mismatches

43;

Inde1s

25;

Gaps

4.5	44	4.3	4.2	41	40	39	38	37	36	(L)	34	. U	) (J	3 1	3 (	2 2	28	
64	64	64	64.5	65	65	65	65	65	65	65	65	65	65	65	66	66	66	
9.3	9.3	9.3	9.4	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5		9.5			9.6	9.6	
380	380	380	332	1012	1012	1012	1012	1012	797	797	797	797	797	276	1012	1012	1012	
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US-08-394-442B-6	US-08-474-988B-6	US-08-416-478A-6	US-09-331-581-23	US-09-031-655-14	US-09-031-655-2	US-08-219-262B-14	US-08-219-262B-2	US-07-944-943-2	PCT-US95-10245-2	US-08-362-240A-2	US-08-288-065A-2	US-08-023-610-2	US-08-663-566A-2	US-08-712-072C-4	US-09-031-655-8	-031-655	US-09-031-655-5	
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## ALIGNMENTS

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; MOLECULE TYPE: protein US-08-330-272-4
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; Patent No. 5985598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-330-272-4
                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 108 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Russo et al
TITLE OF INVENTION: TCL-1 Gene and Protein a
TITLE OF INVENTION: Methods and Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1: CORRESPONDENCE ADDRESS:
                                                                                                                                 TYPE: amino acid
STRANDEDNESS: unk
                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                            TELEFAX: (212) 790-8864/9741
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                     NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
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                                                                                                                   unknown
                                                                                                                                                                                                                                                               (212) 790-9090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                 unknown
25.8%; Score 176.5; DB 2 33.6%; Pred. No. 6.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCL-1 Gene and Protein and Related
                                                                                                                                                                                                                                                                                                                                                                                                              US/08/330,272
                                                                                                                                                                                                                                                                                                               18,872
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                DB 2; Length 108;
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; Sequence 2, Application US/08330272 ; Patent No. 5985598
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                                                US-08-330-272-2
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                                                                                                                                                                                                                                                                                                                                                                        Query Match 25.8%; Score 176.5; DB 5; Length 108; Best Local Similarity 33.6%; Pred. No. 6.5e-14; Matches 43; Conservative 17; Mismatches 43; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: TCL-1 Gene and Protein a TITLE OF INVENTION: Methods and Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 67
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 LVLTYQPE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 SITVHLWOMAVHTRELLSSGOMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSMEQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 S-----HLLT-----SQLPLMWQLYPEERYMDNNSRLWQIQHHLMVRGVQE 98
                                                                                                                                                                          118 LVLTYQPE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 790-8864/9741 TELEFAX: (212) 790-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 LLLKLLPD 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US95/13663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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                                                                                                                                99 LLLKLLPD 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                            58 SITVHLWQMAVHTRELLSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGOIDSMEQ 117
                                                                                                                                                                                                                                                                                                                      1 MASEASVRLGVPPGRLWIQRPGIYEDEEGRTWVTVV---VRFNPSRREWARASQGSRYEP 57
                                                                                                                                                                                                                                                                                                   1 MAGE---DVGAPPDHLWVHQEGIYRDEYQRTWVAVVEEETSFLRARVQQIQVPLGDAARP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
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IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18,872
                                                                                                                                                                                                                                                                                                                                                                                           43; Indels 25; Gaps
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; MOLECULE TYPE: protein US-08-330-272-2
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                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application PC/TUS9513663 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: TCL-1 Gene and Protein at TITLE OF INVENTION: Methods and Compositions
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                            APPLICANT: RUSSO et al
TITLE OF INVENTION: TCI
TITLE OF INVENTION: Met
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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ZIP: 10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 PGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWARASQGSRYEPSITVHLWQMAVHTRE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 PDRLWAWEKFVYLDEKQHAWLPLTIEIKDRLQ------LRVLLRREDVVLGR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/330,272
                                                                                                                                                                                                      ADDRESSEE: Penure & Luncols STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 PMTPTQIGPSLLPIMWQLYPDGRYRSSDSSFWRLVYHIKIDGVEDMLLELLPD 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 LLSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSMEQLVLTYQPE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 21.8%; Score 149; DB 2; Length 113; Local Similarity 29.2%; Pred. No. 1.4e-10;
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                                                                                                                                                          COUNTRY:
                                                                                                                                                                                  STATE:
                                                                                                                                                                                                    CITY: New York
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33; Conservative
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                                                                                                                                         10036
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                                                                                                                                                                              New York
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(212) 79
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                                                                                                                                                             U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
                                                                                                                                                                                                                                           Pennie & Edmonds
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                                                                                                                                                                                                                                                                                  Methods and Compositions
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                                                                                                                                                                                                                                                                                                                        TCL-1 Gene and Protein and Related
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    PCT/US95/13663
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ATTORNEY/AGENT INFORMATION:

FILING DATE: CLASSIFICATION:

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US-08-216-276A-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 55500.
Patent No. 55500.
TakHAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33, Application US/08216276A Patent No. 5595912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 02-AUG-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SNYDER, DAVID TITLE OF INVENTION: SPECI TITLE OF INVENTION: ASSOCITITE OF INVENTION: SEQUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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LENGTH: 113 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 790-8864/974
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                                                                                                                                                                   APPLICATION NUMBER: US 08 FILING DATE: 28-JUN-1993
NAME: Kelber, Steven B. REGISTRATION NUMBER: 30,073
                                                                                                                 APPLICATION NUMBER: FILING DATE: 04-MAY
                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 23-MA
                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 PMTPTQIGPSLLPIMMQLYPDGRYRSSDSSFWRLVYH1KIDGVEDMLLELLPD 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 LLSSGOMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSMEQLVLTYQPE 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 PGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWARASQGSRYEPSITVHLWQMAVHTRE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (211)
TELEX: 66141 PENNIE
TELEX: 700 SEO ID F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
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1755 S. Jefferson Davis Highway, Suite 400
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                                                                                                                 04-MAY-1990
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                                                                                                                                                                                                                                                                                                                                                           Floppy disk
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ASSOCIATED WITH US IBDV VARIANTS, VECTOR CARRYING DNA
SEQUENCES, HOST CARRYING CLONED VECTOR, DEDUCED AMINO ACID
SEQUENCES, VACCINE AND METHOD OF VACCINATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.8%; Score 149; DB 5; Length 113; 29.2%; Pred. No. 1.4e-10; ative 21; Mismatches 45; Indels
                                                                                                                                                                                   US 08/083,784
                                                                        US 07/227,311
                                                                                                                              us 07/519,202
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TITLE OF INVENTION: SPECIF
TITLE OF INVENTION: ASSOCI
TITLE OF INVENTION: SEQUEN
TITLE OF INVENTION: SEQUEN
NUMBER OF SEQUENCES: 34
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                                                                                     APPLICATION NUMBER: US 0//513,202
FILING DATE: 04-MAY-1990
FRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: US 07/227,311
                                                           FILING DATE: 02-AUG-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
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TELEPHONE: (703) 413-2220
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                      NAME: Kelber, Steven B
REGISTRATION NUMBER: 3(
                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 28-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 RLG-----LKLAGPGAFDVNTGPNWATFIKRFPHNPRDWDRLPYLNLPYLPPNAGRQY-- 214
  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/01
FILING DATE: 23-MAR-1994
                                                                                                                                                                                                                                                                                                                                                            COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 RIGVPPGRIMIQRPGIYEDEEGRTWVTVVVRFNPSRREWAR------ASQGSRYEP 57
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1755 S. Jefferson Davis Highway, Suite 400
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2747-054-27 C1P
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GENERAL INFORMATION:
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 31:
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LENGTH: 540 amino acid
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                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
APPLICATION NUMBER: US 07
APPLICATION NUMBER: US 07
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                                                                           FILING DATE: 02-AUG-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/519,202
                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 28-JUN-1993
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ELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 540 amino acids TYPE: amino acid
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STATE: Virginia
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                NAME: Kelber, Steven B.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 27
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                   04-MAY-1990
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                    2747-054-27 CIP
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US-08-216-276A-19
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Best Local Similarity

10.1%; Score 69; DB
23.8%; Pred. No. 11;
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TELEFAX: (703) 413-2220
TELEX: 24865 OPAT UR
INFORMATION FOR SEQ ID NO: 19:
                                                                                                 TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1012 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SNYDER, DAVID B
APPLICANT: MENCEL-WHERSAT, STEPHANIE A
APPLICANT: MENCEL-WHERSAT, STEPHANIE A
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
TITLE OF INVENTION: THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                              REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: QBLON, NORMAN F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         698 RLG-----LKLAGPGAFDVNTGPNWATFIKRFPHNPRDWDRLPYLNLPYLPNAGRQY-- 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          751 ----HLAMAASEFKETPELESAVRAMEAAASVDPL----FQSALSVFMWLEENGIVTDM 801
MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         802 ANFALS 807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 29-MAR
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                           TELEPHONE:
                                                         TYPE: amino acid
STRANDEDNESS: un
                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30; Conservative
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                                       unknown
                                                                                                                                                                                                         (703) 413-3000
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                  protein
                                                                                                                                                                                                                                                                                                                                                             29-MAR-1994
                                                              unknown
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US-08-219-262B-9
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US-08-219-262B-9
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                         Query Match
  Best Local Similarity
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                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2747
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEPAX: (703) 413-2220
TELEPAX: 24855 OPAT UR
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                                                                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1012 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
TITLE OF INVENTION: THEREON
                                                                                  ORGANISM: 1112
ORGANISM: 002-73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     751 ----HLAMAASEFKETPELESAVRAMEAAASVDPL----FQSALSVFMWLEENGIVTDM 801
                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: ur
                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0
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STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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STRAIN: GLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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SNYDER, DAVID B
MENGEL-WHERSAT, STEPHANIE A
                                                                                                                                                                         unknown
                                                                                                           Infectious bursal disease virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Infectious bursal disease virus
                                                                                                                                                      protein
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10.1%;
24.6%;
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Score 69;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                     2747-047-27
DB 1; Length 1012; 11;
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                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 274
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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116 EQLVLT 121
                               751 ----HLAMAASEFKETPELESAVRAMEAAASVDPL-----FQSALSVFMWLEENGIVTDM 801
                                                                                                               698 RLG-----LKLAGPGAFDVNTGPNWATFIKRFPHNPRDWDRLPYLNLPYLPPNAGRQY-- 750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SNYDER, DAVID B
APPLICANT: MENGEL-WHERSAT, STEPHANIE A
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                    58 SITVHLWQMAVHTREL--LSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSM 115
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                                                                                                                                                      8 RLGVPPGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWAR------ASQGSRYEP 57
                                                                                                                                                                                               Match 10.1%; Score 69; DB 1; Length 1012; Local Similarity 23.8%; Pred. No. 11; Length 1012; nes 30; Conservative 18; Mismatches 50; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/219, 262B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 SITVHLWQMAVHTREL--LSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSM 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31; Conservative
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                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Mismatches
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                                                                                                                                                                                               50; Indels 28; Gaps
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                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
TITLE OF INVENTION: THEREON
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08 FILING DATE: 29-MAR-1994 ATTORNEY/AGENT INFORMATION:
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802 ANFALS 807
                                      116 EQLVLT 121
                                                                           751 ----HLAMAASEFKETPELESAVRAMEAAASVDPL-----FQSALSVFMWLEENGIVTDM 801
                                                                                                                                                        698 RLG----LKLAGPGAFDVNTGPNWATFIKRFPHNPRDWDRLPYLNLPYLPPNAGRQY-- 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                  58 SITVHLWQMAVHTREL--LSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSM 115
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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TELEX: 248855 OPAT UR
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                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                               8 RLGVPPGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWAR------ASQGSRYEP 57
                                                                                                                                                                                                                                          30; Conservative 18; Mismatches
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MENGEL-WHERSAT, STEPHANIE A
NVENTION: CHIMBERIC INFECTIOUS BURSAL DISBASE VIRUS
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23.8%; Pred. No. 11
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US-09-031-655-9
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Best Local Similarity 24.6%; Pred. No. 11;
Matches 31; Conservative 16; Mismatches
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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APPLICANT: SWYDER, DAVID B
APPLICANT: MENGEL-WHERSAY, STEPHANIE A
APPLICANT: MENGEL-WHERSAY, STEPHANIE A
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
TITLE OF INVENTION: THEREON
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
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                                                                                                                                                                                   698 RLG-----LKLAGPGAFDINTGPNWATFIKRFPHNPRDWDRLPYLNLPYLPPSAGRQY-- 750
802 ANFALS 807
                                          116 EQLVLT 121
                                                                                       751 ----HLAWAASEFKETPELESAVRAMEAAADVDPL-----FQSALSVFMWLEENGIVTDM 801
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                                                                                                                                    58 SITVHLWQMAVHTREL--LSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHCQIDSM 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/031,655
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                                                                                                                                                                                                                                                                             51; Indels 28;
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; Sequence 12, Application US/09031655 ; Patent No. 6017759

US-09-031-655-12

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RESULT 14
US-08-708-541A-34

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-031-655-12

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEE DATE OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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APPLICATION NUMBER: US 08,
FILING DATE: 29-MAR-1994
ATTORNEY,AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,61
                                                                                                    TITLE OF INVENTION: A METHOD FOR GENERATING BIRNAVIRUS FROM TITLE OF INVENTION: SYNTHETIC RNA TRANSCRIPTS NUMBER OF SEQUENCES: 34
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                                                       NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                              APPLICANT: VAKHARIA, Vikram N. APPLICANT: MUNDT, Egbert
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR CITY: ARLINGTON
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APPLICANT: MENGEL-WHESSAT, STEPHANIE A
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
TITLE OF INVENTION: THEREON
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ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30; Conservative 18; Mismatches 50; Indels 28; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-708-541A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 7, Application US/08219262B
; Patent No. 5788970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: VAKHARIA, VARIAL A APPLICANT: SNYDER, DAVID B APPLICANT: SNYDER, DAVID B APPLICANT: MENCEL-WHERGAT, STEDHANIE A APPLICANT: MENCEL-WHERGAT, STEDHANIE A APPLICANT: MENCEL-WHERGAT INFECTIOUS BURSAL DISEASE VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 34: SEQUENCE CHARACTERISTICS:
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/219,262B
APPLICATION NUMBER: US/08/219,262B
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: KITTS, MODICA C.
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P8
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   754 ALAASEFKETPELEDAVRAMDAAANADP--LFRSALQVFMWLEENGIVTDMANFALS 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               699 RLGMK-----LAGPGAYDINTGPNWATFVKRFPHNPRDWDRLPYLNLPYLPPTAGRQFHL 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                             ALUKESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTAD
STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 AVHTRELLSSGQM--PFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSMEQLVLT 121
                                           FILING DATE:
                         CLASSIFICATION:
                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 202/638-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 9.9%; Score 68; DB 2; Length 1013; Local Similarity 23.1%; Pred. No. 14; Local Similarity 19; Mismatches 61; Indels 19; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20005-5701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 655 Fifteenth Street, N. W., STREET: Suite 330 - G Street Lobby CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 RIGVPPGRIWIQRPGIYEDEEGRTWYTVVVRFNPSRREWARASQ-GSRYEPSITVHIWQM 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/708,541A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                              VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202/638-5000
                                             29-MAR-1994
                                                                                                                                                                                                                                                                                                                                              SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
                                                             US/08/219,262B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61; Indels 10; Gaps
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Database: PIR_68:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Total number of hits satisfying chosen parameters: 219241	Searched: 219241 seqs, 76174552 residues	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Title: US-09-526-329-39 Perfect score: 685 Sequence: 1 MASEASVRLGVPPGRLWIQRHGQIDSNEQLVLTYQPERKD 128	Run on: November 29, 2001, 03:59:59; Search time 18.53 Seconds (without alignments) 526.192 Million cell updates/sec	OM protein - protein search, using sw model	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

Query Match Best Local Similarity 33.6%; Pred. No. 1.90-11; Matches 43; Conservative 17; Mismatches 43; Indels 25; Gaps 4;  Qy 1 MASEASVRLGVPPGRLWIQRPGIYEDEEGRTWVTVVVRENDSRREWARASGGSRYED 57
Co.

25.8 111.6 111.5 1

13826 \$11839 \$11839 \$11839 \$137763 \$030763 \$030760 \$083240 \$083240 \$083240 \$083240 \$083240 \$083275 \$134689

MTCP-1 protein spl
T cell leukemia/ly
viiD2 protein - Ag
dopamine beta-mono
probable transcrip
two-component sens
viiD2 protein - Ag
dopamine beta-mono
probable transcrip
two-component sens
viiD2 protein - Ag
hypothetical 30.1K
probable metallo-o
hypothetical virD2
probable iron-sulf
probable iron-sulf
probable iron-sulf
probable iron-sulf
probable midder
1.4-alpha-glucan b
SHL1 protein - hum
hypothetical prote
embryonic muscle m
conserved hypothet
genome polyprotein
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45	44	43	42	41	40	39	38	37	36	i G	4	ω ω	32	31	30
65	65	65	65.5	65.5	65.5	66	66	66	66	66	66	66	66	66	66.5
9.5	9.5	9.5	9.6	9.6	9.6	9.6	9.6	9.6	9.6	9.6	9.6	9.6	9.6	9.6	9.7
406	352	286	764	350	327	1175	1170	1012	1012	1001	993	536	363	237	1209
2	N	N	N	N	N	2	2	ш	ш	2	$\vdash$	2	N	2	2
C83867	S76078	S48201	D84847	D83102	T15594	T25634	н71295	GNXSCU	GNXSIR	C86181	GNXS98	D83622	T37072	C83183	н85839
dipep	hypothetical prote	licheninase (EC 3.	probable receptor-	a	۳.	hypothetical prote	probable DNA polym	genome polyprotein	genome polyprotein	hypothetical prote	genome polyprotein	arylsulfatase PA01	ь.	probable transcrip	probable regulator

## ALIGNMENTS

18, A	RESULT 2  138286 T cell leukemia/lymphoma protein TCL1 - human N;Alternate names: T-cell leukemia-related protein TCL1 C.Species: Homo sapiens (man) C;Accession: 138286; SS1138 R;Virgilio, L; Narducci, M.G; Isobe, M.; Billips, L.G.; Cooper, M.D.; Croce, C.M.; Proc. Natl. Acad. Sci. U.S.A. 91, 12530-12534, 1994 A;Title: Identification of the TCL1 gene involved in T-cell malignancies. A;Reference number: 138286; MUID:95107991 A;Accession: 138286 A;Molecule type: mRNA A;Residues: 1-114 <ress 1:="" a;cross-references:="" embl.x82240;="" emblx82240;="" nid:9624960:="" pid:9624961="" pid:9624961<="" pidn:caa57708="" th=""><th>GIYEDEEGRTWUTVVVRENPSRREWARASQGSRYJ</th><th>A; Residue: 1-107 <ste> A; Residue: 1-107 <ste> A; Cross-references: EMBL: Z24459; NID: g2252491; PIDN: CAA80828.1; PID: g2252492 C; Genetics: A; Gene: MTCP-1 A; Introns: 35/3; 92/3 C; Keywords: alternative splicing; T-cell proliferation C; Keywords: alternative splicing; T-cell proliferation Query Match Best Local Similarity 33.6%; Pred. No. 1.9e-11; Best Local Similarity 33.6%; Pred. No. 1.9e-11; Matches 43; Conservative 17; Mismatches 43; Indels 25; Gaps 4;</ste></ste></th><th>e form B1 - human ens (man) #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 er, J.; Rosenzwajg, M.; Nakahara, K.; Canki-Klain, N.; Aurias 37, 1993 ovel gene on the human chromosome xq28 translocated to the T</th></ress>	GIYEDEEGRTWUTVVVRENPSRREWARASQGSRYJ	A; Residue: 1-107 <ste> A; Residue: 1-107 <ste> A; Cross-references: EMBL: Z24459; NID: g2252491; PIDN: CAA80828.1; PID: g2252492 C; Genetics: A; Gene: MTCP-1 A; Introns: 35/3; 92/3 C; Keywords: alternative splicing; T-cell proliferation C; Keywords: alternative splicing; T-cell proliferation Query Match Best Local Similarity 33.6%; Pred. No. 1.9e-11; Best Local Similarity 33.6%; Pred. No. 1.9e-11; Matches 43; Conservative 17; Mismatches 43; Indels 25; Gaps 4;</ste></ste>	e form B1 - human ens (man) #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 er, J.; Rosenzwajg, M.; Nakahara, K.; Canki-Klain, N.; Aurias 37, 1993 ovel gene on the human chromosome xq28 translocated to the T
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Result No.

Score

Query Match Length DB

Description

SUMMARIES

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virD2 protein - Agrobacterium tumefaciens plasmid pTiC58
C;Species: Agrobacterium tumefaciens
C;Daecies: Agrobacterium tumefaciens
C;Date: 31-Dec-1993 *sequence_revision 31-Dec-1993 *text_change 08-Oct-1999
C;Accession: S11839; C22666; S12669
R;Rogowsky, P.M.; Powell, B.S.; Shirasu, K.; Lin, T.S.; Morel, P.; Zyprian, E.M.; Steck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 167-174, 'PSWRADEQNVASPSGRSLMPNIGALSGSRLAKSVSKTRIWNSRRRKEIIQNSANLSIH', 'PHLKHF
A;Note: the authors translated the codon ATA for residue 67 as Met and ATA for residue 1
A;Note: this sequence has been revised in reference S11825
C;Genetics:
A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:J03320; NID:g154781; PIDN:AAA91604.1; PID:g154796
R;Hagiya, M.; Close, T.J.; Tait, R.C.; Kado, C.I.
Proc. Natl. Acad. Sci. U.S.A. 82, 2669-2673, 1985
A;Title: Identification of priC58 plasmid-encoded proteins for virulence in Agrobacteriu A;Reference number: A94037; MUID:85190558
A;Accession: C22666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GDB: 250785
A; Map position: 14q32.1-14q32.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid 23, 85-106, 1990
A;Title: Molecular characterization of the vir regulon of Agrobacterium tumefaciens: com
A;Reference number: S11825; MUID:90301800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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               A;Title: Overexpression of virDl and virDl genes in Agrobacterium tumefaciens enhances
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A; Residues: 1-447 < ROG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S11839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                 163 LRIKMAEISLRHG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                109 MFGSGAGGGRYNYLTAFHIDRDHPHLHVVVNRRELLGHGWLKIS-----RRHPQLNYDA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 PGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWARASQGSRYEPSITVHLWQMAVHTRE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PMTPTQTGPSLLPIMWQLYPDGRYRSSDSSFWRLVYHIKIDGVEDMLLELLPD 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 LLSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSMEQLVLTYQPE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 PDRLWAWEKFVYLDEKQHAWLPLTIEIKDRLQ-----LRVLLRREDVVLGR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 ---RASQGSRYEPSITVHL-----WQMAVHTRELLSSGQMPFSQLPAVWQLYPGRKYRA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 LPPDQIHELARSWVQETGTYDESQPDEERQQELTTHIIVSFPAGTSQVAAYAASREWAAE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 VPP-----GRLWIQRPGIYE----DEEGRTWVT--VVVRF-----NPSRREWA-- 47
                                                                                                                                                                                                                                                                                                                                                                                         99 ADSSFWEIA-DHG 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.6%; Score 79.5;
26.3%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 447;
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Qy

3 SEASVRLGVPPGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWARASQGSRYEPSITVH 62

Matches Query Match

Conservative

19; Mismatches

Pred. No.

11.6%; 23.8%;

Score 79.5; DB 2; Length 603;

Best Local Similarity

```
dopamine beta-monooxygenase (EC 1.14.17.1) precursor - human N;Alternate names: dopamine beta-hydroxylase (;Species: Homo sapiens (man) c;Decies: Homo sapiens (man) c;Date: 21.Nov-1993 *sequence_revision 10-Nov-1995 *text_change 08-Oct-1999 c;Accession: S03020; S06283; S61362; I37276 c;Accession: S03020; S06283; S61362; I37276 k;Kurosawa, Y; Fujita, K; Nagatsu, T. Nucleic Acids Res. 17, 1089-1102, 1089 A;Title: Human dopamine beta-hydroxylase gene: two mRNA types having different 3'-ter A;Reference number: S03020; MUID:89160241
C;Superfamily: peptidylglycine monooxygenase I homology
C;Keywords: catecholamine biosynthesis; copper; glycoprotein; monooxygenase; oxidored
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-603/Product: dopamine beta-hydroxylase #status predicted <MAT>
F;282-505/Domain: peptidylglycine monooxygenase I homology <PGMD
                                                                                                                                                                                                                                                                                                                                                        A;Note: part of this sequence was confirmed by protein sequencing A;Note: 502-Leu and 507-Gly were also found R;Li, B; Tsing, S; Kosaka, A.H; Nguyen, B; Osen, E.G.; Bach, C.; Chan, H; Barnet Biochem. J. 313, 57-64, 1996
A;Title: Expression of human dopamine beta-hydroxylase in Drosophila Schneider 2 cell A;Title: Expression of human dopamine beta-hydroxylase in Drosophila Schneider 2 cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBO J. 6, 3931-3937, 1987
A;Title: The primary structure of human dopamine-beta-hydroxylase: insights into the A;Reference number: S06283; MUID:88166633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X13255; NID:g30473; PIDN:CAA31631.1; PID:g30474
A;Note: 304-Ser and 535-Cys were also found; the amino acid exchange at residue 535 w
A;Note: the authors translated the codon TGC for residue 380 as Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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A; Residues: 1-447 <WAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-196, 'T',198-534,'C',536-603 <LAM>
A;Cross-references: EMBL:Y00096; NID:g30455; PIDN:CAA68285.1; PID:g30456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Lamouroux, A.; Vigny, A.; Biguet, N.F.; Darmon, M.C.; Franck, R.; Henry, J.P.; Mall EMBO J. 6, 3931-3937, 1987
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                                                                                                                                                                                                          A; Molecule type: protein A; Residues: 26-34 < LIB>
                                                                                                                                                                                                                                                                                           A; Accession: S61362
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                                                                                                                                                                                                                                                                                                                              A; Reference number: S61362; MUID: 96132606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 LRIKMAEISLRHG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 ADSSFWEIA-DHG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 ---RASQGSRYEPSITVHL-----WQMAVHTRELLSSGQMPFSQLPAVWQLYPGRKYRA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 LPPDQIHELARSWVQETGTYDESQPDEERQQELTTHIIVSFPAGTSQVAAYAASREWAAE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 VPP-----GRLWIQRPGIYE----DEEGRTWVT--VVVRF-----NPSRREWA-- 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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A; Residues: 1-476 <STO>
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                                                                                                                                                                                                                                                                                    A;Gene;
                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BAB04892.1; GSPDB:GN0
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A83650; MUID: 20263314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: 083240
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: E83796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
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A; Molecule type: DNA
A; Residues: 1-238 <STO>
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: C83240
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A; Accession: C83240
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                                                                                                                                                      Query Match 11.0%; Score 75.5; DB 2; Length 476; Best Local Similarity 27.7%; Pred. No. 4.1;
                                                                                                                                                                                          Query Match
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115 OSRGRYELSYNGATIFYVVTKFNSFGREGYLISYMWDTYRDSMVNRLWERLLYIL-LLSS 173
                                                     19 QRPGIYE-DEEGRTWVTVVVRFNPSRRE-WARASQGSRYEPSITVHLWQMAVHTRELLSS 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 AMVSEQGRVPATEVLSARQMPASAAVCELLELPALSSVYQIRRARRVDGRLVLYVEH 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 QMA-----VHTRELLSSCQMPFS-----QLPAVWQLYPGRKYRAADSSFWEIADH 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 ATTRITLREALIQLESQGLIYREE------RRGWFVSPERLAYNPLVRSHFH 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                    BH1173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 ASVRLGVPPGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWARASQGSRYEPSITVHLW 64
                                                                                                                                  36; Conservative
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                                                                                                                 16; Mismatches 53; Indels 25; Gaps
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                       В
                                                                                                                                                                                                                                                                                              A; Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-261 <KAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               k, Title: Nucleotide sequence of a regulatory region controlling alginate synthesis in A, Reference number: JQ0132; MUID:90108714 A, Recession: JQ0137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Species: Pseudomonas aeruginosa
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 07-Jun-1996
C:Accession: JQ0137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Kato, J.; Chu, L.;
Gene 84, 31-38, 1989
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Mol. Gen. Genet. 213, 229-337, 1988
A;Title: Organization and characterization of the virCD genes from Agrobacterium rhiz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        virD2 protein - Agrobacterium rhizogenes plasmid pRiA4b
C;Species: Agrobacterium rhizogenes
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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A; Residues: 1-436 <HIR>
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                                                                                                                                               Matches
                                                                                                                                                                             Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.9%; Score 74.5; DB 2; Length 436; Best Local Similarity 25.6%; Pred. No. 4.7; Matches 34; Conservative 17; Mismatches 43; Indels 39; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 MFGSGAGGGSYNYLTAFHIDRDHPHLHYVVNRRELLGHGWLKIS-----RRHPQLNYDA 162
   51 PKQRWRRLPGRWESPQRSQQERWRAWLRQVSRLRVSPQAWPPVSPQRSQPAWLQASR--P 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 LRINMAEISLRHG 175
                                                                  13 PGRLWIQRPGIYE-----DEEGRTWVTVVVRFNPSRREWARAS------QGSRYEP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 NLVRYDQSQK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 LVLTYQPERK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 A---LSLLPAIWLKHYLRQPLILLGNRLEQIADRNWKEPFKWEGDEDFQKLSNQFERMRQ 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 ---RASQGSRYEPSITVHL-----WQMAVHTRELLSSGQMPFSQLPAVWQLYPGRKYRA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 VPP-----GRLWIQRPGIYE----DEEGRTWVT--VVVRF------NPSRREWA-- 47
                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 ADSSFWEIA-DHG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 LPPDQIHELARSWVQETGTYDESQPDEERQQELTTHIIVSFPAGTSQAAAYAASREWAAE 108
                                                                                                                                                                                                                                                                                                                                                    3-Met could also be the initiator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 GOMPFSQLPAVWQ------LYPGRKYRAADSSF-----WEIAD-----HGQIDSMEQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
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                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L.; Kitano, K.; DeVault, J.D.; Kimbara, K.; Chakrabarty, A.M.; Misra
                                                                                                                           10.7%; Score 73.5; DB 2; Length 261; 27.0%; Pred. No. 3.2; ative 11; Mismatches 41; Indels 29
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A; Note: plasmi
C; Genetics:
A; Gene: virD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical virD2 protein - Agrobacterium tumefaciens plasmids
(;Species: Agrobacterium tumefaciens
(;Species: Agrobacterium tumefaciens
C;Date: 31-Mar-1988 *sequence_revision 31-Mar-1988 *text_change 08-Oct-1999
C;Accession: B29826; B25063
C;Accession: B29826; B25063
C;Accession: B29826; R.K.; Gelvin, s.B.; Silghtom, J.L.
R;Jayaswal, R.K.; Veluthambi, K.; Gelvin, s.B.; Silghtom, J.L.
J. Bacteriol. 169, 5035-5045, 1987
J. Bacteriol. 169, 5035-5045, 1987
A;Title: Double-stranded cleavage of T_DNA and generation of single-stranded T-DNA molec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A;Reference number: A82950; MUID:20437337
A;Accession: G83175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable metallo-oxidoreductase PA3768 [imported] – Pseudomonas aeruginosa (strain PAOl)
C;Species: pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-463 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession:
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                                                                                                                                                                                                                                                                                                   R:Yanofsky, M.F.; Porter, S.G.; Young, C.; Albright, L.M.; Gordon, M.P.; Nester, E.W. Cell 47, 471-477, 1986
A:Title: The virD operon of Agrobacterium tumefaciens encodes a site-specific endonuclea
                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-424 <JAY>
A;Residues: 1-424 <JAY>
A;Cross-references: EMBL:M17989; NID:g142288; PIDN:AAA22114.1; PID:g142290
A;Note: plasmid pTiA6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain PAO1
A;Genome: plasmid
C;Keywords: endonuclease
                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-424 < YAN>
                                                                                                                                                                                                                                                                         A; Reference number: A90886; MUID:87028239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A91846; MUID: 88032822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
                                                                                                                                                                                                                                           Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: B2982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 RVSPHAWPPA-----WLRASRLRFS--PRAWPPVSPQASPPAWLRASRLRF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 FKTQDAGSYWY --- HPHLMSSEQL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 SITVHLWQMAVHTRELLSSGQMPFSQLPAVW-----QLYPGRKYRAADSSF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 YRAADS-SEWEIADHGQIDSMEQL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 RAKQGEWLRVRFTNRLDEPTTIH-WH---GIRLPIEMDGVPYISQPPV---QPGESFIYQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 NPSRREWARASQGSRYEPSITVHLWQMAVHTRELLSSGQMPFSQLPAVWQLYPGR----K 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 LAGLAVVGLGAGGARLWLARPQVAQEYDYELIAAPLDLEIVPGFSSPALAYGGQCPGVEL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Госат
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MASEASVRLGVPPGRLWIQRPGI----YEDEEGRTWVTVV------VRF 39
                                                                                                                                      plasmid pTiA6NC
                             plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                           B25063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.7%; Score 73; DB 2; Length 463; 24.3%; Pred. No. 7.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55; Indels 36; Gaps
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probable iron-sulfur binding oxidoreductase - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999 (C;Accession: T34689)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QΥ
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A; Accession: T34689
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C;Superfamily: Mycobacterium tuberculosis mbtB protein; acetate--CoA ligase homology; C;Keywords: carrier protein
F;5-74/Domain: acyl carrier protein homology <ACP>
F;598-1037/Domain: acetate--CoA ligase homology <ACP>
F;1060-1131/Domain: acetate--CoA ligase homology <ACP1>
F;1189-1400/Domain: acyl carrier protein homology <ACP1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 03-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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A; Residues: 1-513 <HAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:281371; GB:AL123456; NID:g3261669; PIDN:CAB03756.1; PID:g16573
                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-1414 < COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: B70674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable mbtB protein - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: strain A3(2)
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                                                                                                                                                                                                                              A;Gene: mbtB
                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: B70674
                                                                                                                                                                                                                                                                                    A; Experimental source: strain H37Rv
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Best Local 9
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      436 LPPGEGAVVRAGGGRLAVYRDEEGALHAVSPRCTHLGCLVDFNAAERAWECPCHGSRF 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 MAEISL----RHGIVLDATSRAERGIAERPITYAEHRR 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 MFGSGYGGGRYNYLTAYHVDRDHPHLHVVVNRRELLGHGWLKISRRHP--QLNYDGLRKK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 VPPGRL-----WIQRPGIYE----DEEGRTWVT--VVVRF-----NPSRREWARA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 VPPGRLWIQRPG----IYEDEEGR-----TWVTVVVRFNPSRREWARASQGSRY 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 AADSSFWEIADHGQI-----DSMEQLVLTYQPERK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 VPPDQIRELAQSWVTEAGIYDESQSDDDRQQDLTTHIIVSFPAGTDQTAAYEASREWAAE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 SQGS-----RYEPSITVHL-----WQMAVHTRELLSSGOMPFSQLPAVWQL-YPGRKYR 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.6%; Score 72.5; D. 32.8%; Pred. No. 9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24; Mismatches 49; Indels 47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Mismatches 19; Indels 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.; Holroyd,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gordon
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A;Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-g
A;Pathway: glycogen/starch biosynthesis
C;Superfamily: 1,4-alpha-glucan branching enzyme
                                                                                                             A;Cross-references: EMBL:Y08786; NID:g1621011; PIDN:CAA70038.1; PID:g1621012 A;Experimental source: cv. Dianella; cell line Dianella C;Genetics: A;Gene: sbeI C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                     R;Khoshnoodi, J.; Blennow, A.; Ek, B.; Rask, L.; Larsson, H. Eur. J. Biochem. 242, 148-155, 1996
A;Title: The multiple forms of starch branching enzyme I in Solanum tuberosum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000 C;Accession: T07824
                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-830 <KHO>
                                                                                                                                                                                                                                                                                                                                                                       A:Reference number: Z16155; MUID:97112484
A:Accession: T07824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QΥ
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C; Superfamily: NADPH dehydrogenase chain OYE2
                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1,4-alpha-glucan branching enzyme (EC 2.4.1.18) I (clone sbeI7) - potato (fragment) C.Species: Solanum tuberosum (potato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE004426; GB:AE003853; NID:99658431; PIDN:AAF96889.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype E1 Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-367 <HEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833 A;Accession: C82391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: C82391
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C82391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 IA--PSA-----LKPVETQVW-IADEQGNGQMVDCVEPRAMT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                922 TWYRTGDLARYWHDGTLEFVGRADH-RVKISGYRVELGEIEAALQRLPGVHAAAA 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   862 ASVPYGVPFPNNACRVVADSGDDCPDWVAGELWVSGRGIARGYRGRPELTAERFVEHDGR 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 FSQLPAVWQLYPGRKYRAADSSFWEIAD---HGQ-IDSMEQLVLT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 PGVYTDEQTSGWKTVT-----QAVKQQGA----AMFCQLWHVGRVSHPVFQKGQLP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 PGIYEDEEGRTWVTVVVRFNPSRREWARASQGSRYEPSITVHLWQMAVHTRELLSSGQMP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 EWARASQGSRYEPSITVHLWQMAVHTRELLSSGQMPFSQLPAVWQLYPGRKYRAA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .ch 10.2%; Score 70; DB 2; Length 367; Ll Similarity 24.8%; Pred. No. 11; 26; Conservative 18; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28; Gaps
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밁 δÃ 밁 C; Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase Matches Query Match 545 WIDFP-----REGNNW-----SYDKCRRQWNLADSEHLRYK---FMNAFDRAMNSLDEKF 591 652 WEFGGHGR 659 592 SFLASGKQIVSSMDDDNKVVVFERGDLVFVFNFHPKNTYEGYKYGCDLPGKYRVALDSDA 651 104 WEIADHGQ 111 73 -LLSSGQMPFS-------QLPAVWQLYPGR-----KYRAA-DSSF 103 17 WIQRPGIYEDEEGRTWVTVVVRFNPSRREWARA-SQGSRYEPSITVHLWQMAVHTRE--- 72 31; Conservative 17; Mismatches 34; Indels 46; Gaps

Search completed: November 29, 2001, 04:04:10 Job time: 251 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLB3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
olso40 homo sapien p0864 avian infec p46971 saccharomyc p52519 avian infec p52519 avian infec p52519 avian infec p52523 mycobacteri O9nyv4 homo sapien p37247 bacteroides p51691 pseudomonas p25220 avian infec p15480 avian infec p2331 avian infec p2331 avian infec p24764 synechococc p56273 thiobacillu
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P56845 mus musculu
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P56879 homo sapien
P18592 agrobacteri
P09172 homo sapien
P13462 agrobacteri
P13468 agrobacteri
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1 MASEASVRLGVPPGRLW1QRPGIYEDEEGRTWVTVVVRFNPSRREWARASQGSRYEPSIT 60

100.0%; Score 685; DB 1; Length 128; 100.0%; Pred. No. 1e-65; ative 0; Mismatches 0; Indels

0; Gaps

0;

Query Match 100. Best Local Similarity 100. Matches 128; Conservative

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winis SMJSS-PROT entry is copbetween the Swiss Institute the European Bioinformatics use by non-profit institute modified and this statement entities requires a license or send an email to licensee send an email to licensee send an email to licensee entities, AF110465; AAD16997.1; EMBL; AF110465; AAD16996.1; EMBL; AF17027; AAD30130.1; HSSP; P56278; IAIX. HSSP; P56278; IAIX. HSSP; P56278; TCL1_MTCP1 rorbom; PD01575; TCL1_MTCP1 Proto-oncogene; Chromosomal SEQUENCE 128 AA; 14846 MW	AAN SH	E. F. F. 383333	666 666 666 666 666 666 666 666 666 66
O'O' entry Swiss lns Bioinform profit i this stat iires a li iail to li iires a li iires	ROM N.A.  178995; Pubme  178995; Pubme  1880; Hallas C.,  ties at 14932  ",  Acad. Sci.  ROM N.A.  Mendelson C.R  otrophoblast  otrophoblast sub  (MAR-1999) to  SPECIFICITY  SPECIFICITY  SPECIFICITY  RITY: BELONGS  RITY: BELONGS  RITY: BELONGS	N STANDJ O (Rel. 39 DO (Rel.	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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ute of section with the comparison of the compar	ISODE N. 1 in T. 1. i	Created) Last seg Last and MA PROTE PECIFIC Ordata; imates;	
ght. It is Bioinforma Elioinforma titute Th ns as long ns as long ement (See -sib.ch).	maligna maligna 19-2951( 19-2951) 19-2951( 19-2951) 19-2951( 19-2951) 19-2951( 19-2951) 19-2951( 19-2951) 19-2951( 19-2951)	PRT; 124 ) quence upda nocation up EIN 118 (TCI EIN 718 (TCI PROTEIN) ( PROTEIN) ( Craniata; Catarrhini	GUB_RHOMR HCYA_OCTDO TYE_RAT AC48_MOUSE MED_ECOLI PARB_XYLFA LAG3_HUMAN MOX1_SCHPO MOX1_SCHPO MOX1_SCHPO LORSA_HUMAN CPSA_HUMAN CPSA_HUMAN CPSA_HOMAN
ced through a coll and the EMBL out re no restriction ts content is in age by and for c://www.isb-sib.ch/	mancies involve two  (1(1999). \(\hat{\chi_{\chi}}\chi_{\chi\ti}}\chi_{\chi_{\chi_{\chi_{\chi_{\chi_{\chi_{\chi_{\chi_{\chi\ti}}\chi_{\chi\ti}}\chi_{\chi_{\chi_{\chi_{\chi_{\chi_{\chi_{\chi_{\chi_{\chi\ti}}\chi_{\chi}\chi_{\chi_{\chi_{\chi_{\chi_{\chi_{\chi_{\chi_{\chi_{\chi_{\chi\}\chi_{\chi_{\chi_{\chi_{\chi_{\chi_{\chi_{\chi_{\chi}\chi_{\chi_{\chi_{\chi_{\chi}\chi_{\chi_{\chi}\chi_{\chi_{\chi}\chi_{\chi}\chi_{\chi_{\chi}\chi_{\chi_{\chi_{\chi_{\chi_{\chi_{\chi}\chi}\chi_{\chi}\chi_{\chi}\chi_{\chi}\chi_{\chi}\chi}\chi_{\chi}\chi}\chi_{\chi}\chi}\chi_{\chi}\chi_{\chi}\chi_{\chi}\chi}\chi_{\chi}\chi}\chi_{\chi}\chi}\chi_{\chi}\chi}\chi}\chi\chi\chi}\chi\chi\chi}\chi\chi}\chi\chi\chi\chi}\chi\chi\chi}\chi\chi\chi\chi\chi}\chi}	3 AA. ate) Jdate) Jdate) (SYN-1). (SYN-1). Vertebrata; Euteleostomi; Hominidae; Homo.	P45798 rhodothermu P12659 octopus dof P42533 rattus norv O97034 mus musculu P30958 escherichia G9pb63 xylella fas P18627 homo sapien O90878 schizosacch O00097 ictalurid h P46551 caenorhabdi Q10570 homo sapien Q10569 bos taurus

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TLB4_MOUSE
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DT 30-MAY
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DE TCL1B4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; EuleieOScolli;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TCL1B4 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genomic analysis of human and mouse TCL1 loci reveals a complex of tightly clustered genes.";
Proc. Natl. Acad. Sci. U.S.A. 96:14418-14423(1999).
-i- SIMILARITY: BELONGS TO THE TCL1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF195488; AAF12801.1; -.
MGD; MGI:1351601; TC11b1.
InterPro; IPR002709; TCL1_MTCP1.
ProDom; PD015575; TCL1_MTCP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hallas C., Pekarsky Y., Itoyama T., Varnum J., Bichi R., Rothstein J.L., Croce C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20056259; PubMed-10588720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
    TCL1B4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TYQPERKD 128
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                                                                                                                         TLB4_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 VHLWQMAVHTREILSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSMEQLVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VHLWQWAVHTRELLSSGQWPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSMEQLVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 VHLWKLI--PQQVIPENPLNYDELPTTWKLESRNIYWATDGTHWRLLDHSQLGDTEQLIL 111
                                                                                                                                                                                                                                                                   61 VHLWQMAVHTRELLSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSMEQLVL 120
                                                                                                                                                                                                                                                                                                           1 MAAAAFDPLGPLPVYLVSVRLGIYEDEHHRVWIVANV-----ETSHSSHGNRRRTHVT 53
                                                                                                                                                                                                                                                                                                                                              1 MASEASVRLGVPPGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWARASQGSRYEPSIT 60
                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                      41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 AA; 13432 MW;
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                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                            26.1%; Score 178.5; DB 1 34.2%; Pred. No. 3.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                          19; Mismatches
                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5D2E08EBC7BE2A64 CRC64;
                                                                                                                              120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 116;
                                                                                                                                                                                                                                                                                                                                                                                               51;
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                                                                                                                                                                                                                                                                                                                                                                                               9;
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               MTC2_MOUSE
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                          with t(X;14) translocations.";

Blood 87:1923-1927(1996).

-i. ALTERNATIVE PRODUCTS: ALTERNATIVE SPLICING PRODUCES TWO SHORT, YET COMPLETELY DIFFERENT PROTEINS. THE LONGER PRODUCT, TYPE-BL, IS KNOWN AS P13 MTCP-1 (AC Q619045). THE SHORTER PRODUCT, TYPE-A, IS KNOWN AS P8 MTCP-1 (AC Q61908).

-i. TISSUE SPECIFICITY: NOT FOUND AT A SIGNIFICANT LEVEL IN ANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:1351604; Tcllb4.
InterPro; IPR002709; TcLl_MTcl
ProDom; PD015575; TcLl_MTcP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE B1) (P13MTCP1).
MTCP1 OR C6.1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q60945;

Q1-NOV-1997 (Rel. 35, Created)

Q1-NOV-1997 (Rel. 35, Last sequence update)

Q1-MAY-2000 (Rel. 39, Last annotation update)

P13 MTCP-1 PROTEIN (MATURE T-CELL PROLIFERATION-1 TYPE B1) (MTCP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF195492; AAF12805.1; -.
                                                                                                                                                                   Madani A., Choukroun V., Soulier J., Cacheux V., Claisse J.-F., Valensi F., Daliphard S., Cazin B., Levy V., Leblond V., Daniel M.-T., Sigaux F., Stern M.-H.; Expression of plaMTCPl is restricted to mature T-cell proliferations
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Veriebraid; Euleieoscomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
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                                                                                                                                                                                                                                                        MEDLINE=96202516; PubMed=8634440;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 LWQMTTLFQEPSPDSLKTFNFLPRTWRLESRNTYRGADAMHWRLVNHSQFYGTEELVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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Hallas C., Pekarsky Y., Itoyama T., Varnum J., Bichi R.,
Rothstein J.L., Croce C.M.;
"Genomic analysis of human and mouse TCL1 loci reveals a complex of
"Genomic analysis of human and mouse TCL1 loci reveals a complex of
tightly clustered genes.";
Proc. Natl. Acad. Sci. U.S.A. 96:14418-14423(1999).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
63 LWQMAVHTRELLSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSMEQLVL 120
                                                                                   4 SVRFPCMPFPPCFLVCTRDDIYEDEHGROWVAAKVETS-----SHSPYCSKIETCVTVH 57
                                                                                                                                                                       6 SVR----LGVPPGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWARASQGSRYEPSITVH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 ĀA; 14123 MW; 7F58E0AEBFF3F339 CRC64;
                                                                                                                                                                                                                                                                                                26.1%; Score 178.5; DB 1; 36.4%; Pred. No. 3.7e-12;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98188217; PubMed=9520380;
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*MTCP-1: a novel gene on the human chromosome Xq28 translocated to the tech receptor alpha/delta locus in mature T cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
15-UUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
Pl3 MTCP-1 PROTEIN (MATURE T-CELL PROLIFERATION-1 TYPE B1) (MTCP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE B1) (P13MTCP1). MTCP1 OR C6.1B.
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P56278;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Incogene 8:2475-2483(1993).
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SEQUENCE 107 AA; 12645 MW; 7996813A182C2308 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01840; TCL1_MTCP1; 2. ProDom; PD015575; TCL1_MTCP1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002709; TCL1_MTCP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SIMILARITY: BELONGS TO THE TCL1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59
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                                                                                                                                                                                              P-1 in T cell malignancies.";
c. Natl. Acad. sci. U.S.A. 95:3413-3418(1998).
ALTERNATIVE PRODUCTS: ALTERNATIVE SPLICING PRODUCES TWO SHORT, YET COMPLETELY DIFFERENT PROTEINS. THE LONGER PRODUCT, TYPE-B1, IS KNOWN AS P13 MTCP-1 (AC P56278). THE SHORTER PRODUCT, TYPE-A, IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
DISEASE: DETECTED IN T-CELL LEUKENIA BEARING A T(X;14)
TRANSLOCATION. PLAYS A KEY ROLE IN T-CELL PROLYMPHOCYTIC LEUKENIA
                                                                                                                                   KNOWN AS P8 MTCP-1 (AC P56277).
TISSUE SPECIFICITY: NOT FOUND AT A SIGNIFICANT LEVEL IN ANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 VGAPPDHLWVHQEGVYRDEYQRTWVAVVEEETSFLKARVQQVQVPLGDATKPS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 LGVPPGRLWIQRPGIYEDEEGRTWVTVV---VRFNPSRREWARASQGSRYEPSITVHLWQ 65
                                                                                                                TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----HLLT-----SQLPLMWQLYPEERYMDNNSRLWQIQHHLMVRGVQELLLKLLPD 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P56278; 1A1X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.0%; Score 178; DB 1; Length 107; 32.5%; Pred. No. 3.6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
ProDom; PD015575; TCL1_MTCP1; 1.
                               EMBL; AF195490; AAF12803.1; -. MGD; MGI:1351600; Tc11b3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
                 MGD; MGI:1351600; TC11b3.
InterPro; IPR002709; TCL1_MTCP1.
                                                                                           Or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                             tightly clustered genes.";
Proc. Natl. Acad. Sci. U.S.A. 96:14418-14423(1999).
                                                                                                                                                                                                                                                                                                                        Hallas C., Pekarsky Y., Itoyama T., Varnum J., Bichi R. Rothstein J.L., Croce C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P56842;
30-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20056259; PubMed=10588720;
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCL1B3 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                '!- SIMILARITY: BELONGS TO THE TCL1 FAMILY
                                                                                                                                                                                                                                                                                                   Genomic analysis of human and mouse TCL1 loci reveals a complex of
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLB3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proto-oncogene; Chromosomal translocation; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 300116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 224459; CAA80828.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 LVLTYQPE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002709; TCL1_MTCP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 S------HLLT-----SQLPLMWQLYPEERYMDNNSRLWQIQHHLMVRGVQE 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 SITVHLWQMAVHTRELLSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSMEQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAGE---DVGAPPDHLWVHQEGIYRDEYQRTWVAVVEEETSFLRARVQQIQVPLGDAARP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MASEASVRLGVPPGRLWIQRPGIYEDEEGRTWVTVV---VRFNPSRREWARASQGSRYEP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1A1X; 27-MAY-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                         lia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 AA; 12600 MW; C00967E1AECDDDCA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.8%; Score 176.5; 33.6%; Pred. No. 5.2
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TCLA_MOUSE
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Narducci M.G., Virgilio L., Engiles J.B., Buchberg A.M., Billips L., Facchiano A., Croce C.M., Russo G., Rothstein J.L.;
"The murine Tcl1 oncogene: embryonic and lymphoid cell expression.";
oncogene 15:919-926(1997).
-- SUBCELLULAR LOCATION: MICROSOMAL FRACTION (BY SIMILARITY).
-- SIMILARITY: BELONGS TO THE TCL1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
T-CELL LEUKEMIA/LYMPHOMA PROTEIN 1A (P14 TCL1 PROTEIN) (TCL1 ONCOGENE)
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1097156; Tcll.
Interpo; IPR002709; TCLL_MTCP1.
Pfam; PF01840; TCLL_MTCP1; 2.
ProDom; PD015575; TCL1_MTCP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCL1A OR TCL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P56280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF031956; AAB87461.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCLA_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
119 VL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 PPGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWARASQGSRYEPSITVHLWQMAVHTR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 EPTPQQPINNNSLPTMWRLESMNTYTGTDGTYWRLLDHSQMGDTLQLIL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 ELLSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSMEQLVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 PPRFLYCTRDDIYEDENGRQWYVAKV-----ETSRSPYGSRIETCITVHLQHMTTIPQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                    45 FQVILRQEDVTLGEAMSPSQLVPYELPLMWQLYPKDRYRSCDSMYWQILYHIKFRDVEDM 104
                                                                                                  59 ITVHLWQMAVHTRELLSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSMEQL 118
                                                                                                                                                                                                              1 MASEASVRLGVP--PGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWARASQGSRYEPS 58
                                                                                                                                                            1 MATQRAHRAETPAHPNRLWIWEKHVYLDEFRRSWLPVVIKSN--
                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                     40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y15376; CAA75599.1;
P56279; 1JSG.
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                                                                                                                                                                                                                                                                                                                                                                                                     116 AA; 14112 MW; 46DEED2F973F389A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 AA; 14170 MW;
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                                                                                                                                                                                                                                                                     Conservative 20; Mismatches 44; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                               24.7%; 32.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.6%; Score 175.5; 36.7%; Pred. No. 7.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 7.8e-12
                                                                                                                                                                                                                                                                                                  Score 169; DB 1;
Pred. No. 3.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BD1501F81C24F230 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 AA.
                                                                                                                                                                                                                                                                                                                            DB 1; Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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        RRY OCC
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                                                                                                                                                                                                                                                                                                                               TLB2_MOUSE
P56841;
30-MAY-2000
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TLB5_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P56845;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCL1B5 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Multigene family.
SEOUENCE 121 AA; 13668 MW; 32815CCD629B4297 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20056259; PubMed=10588720;
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                                  SEQUENCE FROM N.A.
MEDLINE=20056259; PubMed=10588720;
                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR002709; TCL1_MTCP1.
ProDom; PD015575; TCL1_MTCP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:1351635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 96:14418-1442
- i- SIMILARITY: BELONGS TO THE TCL1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tightly
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  Hallas C., Pekarsky Y., Itoyama T., Varnum J., Bichi R.,
                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                                                                                       TCL182 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF195493; AAF12806.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 LPQEPTPQQPINNNSLPTMWRLESRNTYTGTDGTYWRLLDHSQMGDTVQLTL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 QRP-----GIYEDEEGRTWVTVVVRFNPSRREWARASQGSRYEPSITVHLWQMAV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 HTRELLSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSMEQLVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 QRPLPVLLVSVSLGIYEDEHHRVWIAVNV-----ETSHSSHGNRIETCVTVHLQHMTT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clustered genes."
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                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.9%; Score 163.5; DB 1; Length 121; 33.0%; Pred. No. 1.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S.A. 96:14418-14423(1999).
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                                                                                                                                                 Murinae; Mus
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TCLA_HUMAN
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                            "Crystal structure of pl4TCL1, an oncogene product involved in T-cel1 prolymphocytic leukemia, reveals a novel beta-barrel topology."; Structure 6:147-155(1998).
                                                                                   MEDLINE-98179932; PubMed-9519406;
Hoh F., Yang Y.-S., Guignard L., Padilla A., Stern M.-H.,
Lhoste I.-M., van Tilbourgh H.;
                                                                                                                                                                                                                                      CHARACTERIZATION, AND LOCALIZATION. MEDLINE=95079394; PubMed=7987816;
                                                                                                                                                                                                                                                                                                                              Virgilio L., Narducci M.G., Isobe M., Billips L.G., Cooper M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Last annotation update)
T-CELL LEUKEMIA/LYMPHOMA PROTEIN 1A (P14 TCL1 PROTEIN) (TCL1 ONCOGENE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation updat
     - 1 - SUBCELLULAR LOCATION: MICROSOMAL FRACTION
                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                  Fu T.-B., Virgilio L., Narducci M.G., Facchiano A., Russo G.,
                                                                                                                                                                                                                                                                                 "Identification of the TCL1 gene involved in T-cell malignancies.";
Proc. Natl. Acad. Sci. U.S.A. 91:12530-12534(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCLA_HUMAN
P56279;
                                                                                                                                                                        lancer Res. 54:6297-6301(1994)
                                                                                                                                                                               "Characterization and localization of the TCL-1 oncogene product.";
                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95107991; PubMed=7809072;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCL1A OR TCL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TCL-1 PROTEIN).
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InterPro; IPR002709; TC11_MTCP1.
ProDom; PD015575; TC11_MTCP1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF195489; AAF12802.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 96:14418-14423(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genomic analysis of human and mouse TCL1 loci reveals a complex of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rothstein J.L., Croce C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 QMTRYPQEPAPYNPMNYNFLPMTWRLASMNTYRGTDAMHWRLLNHSQVGDTVQLIL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 QMAVHTRELLSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADHGQIDSMEQLVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 GVPPGRLWIQ-----RPGIYEDEEGRTWVTVVVRFNPSRREWARASQGSRYEPSITVHLW 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Loca1
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                           SUBUNIT: HOMODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AA; 13672 MW; A6B0851165E9B0AA CRC64;
                                                                                                                                                                                                                                                                                                                         Russo G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.1%; Score 158.5; DB 1 31.0%; Pred. No. 4.7e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 117;
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Query Match
Rogowsky P.M., Powell B.S., Shirasu K., Lin T.-S., Morel P., Zyprian E.M., Steck T.R., Kado C.I., "Molecular characterization of the vir regulon of Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VID2_AGRT5 STANDARD; PRT; 447 AA
F18592; P06521; P06522;
O1-JAN-1988 (Rel. 06, Created)
O1-NOV-1990 (Rel. 16, Last sequence update)
O1-AUG-1992 (Rel. 23, Last annotation updat
                                                                                                                                         MEDLINE=85190558; PubMed=2986128;
Hagiya M., Close T.J., Tait R.C., Kado C.I.;
"Identification of pric58 plasmid-encoded proteins for virulence
                                                                                                                                                                                                                                               PRELIMINARY SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                       tumefaciens: complete nucleotide sequence and gene organization of the 28.63 kbp regulon cloned as a single unit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-90301800; PubMed-2194232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid pTiC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T-DNA BORDER ENDONUCLEASE VIRD2 (EC 3.1.-.-).
                                                                                                                                                                                                                                                                                                       Plasmid 23:85-106(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD015575; TCL1_MTCP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002709; TCL1_MTCP1.
Pfam; PF01840; TCL1_MTCP1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 186960;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SIMILARITY: BELONGS TO THE TCL1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PMTPTQIGPSLLPIMWQLYPDGRYRSSDSSFWRLVYHIKIDGVEDMLLELLPD 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 LLSSGQMPFSQLPAVWQLYPGRKYRAADSSFWETADHGQIDSMEQLYLTYQPE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 PDRIMAWEKFVYLDEKQHAWLPLTIEIKDRLQ-------LRVLLRREDVVLGR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 PGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWARASQGSRYEPSITVHLWQMAVHTRE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THYMOCYTES AND ACTIVATED PERIPHERAL LYMPHOCYTES. PREFERENTIALLY EXPRESSED EARLY IN T-AND B-LYMPHOCYTE DIFFERENTIATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAR-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chromosomal translocation; Microsome; 3D-structure. AA; 13459 MW; 90D55ABC97C36D04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.8%; Score 149; DB 1; 29.2%; Pred. No. 4.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         447 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way because the content of the content of
                                                                                                            "The primary structure of human dopamine-beta-hydroxylase: insiginto the relationship between the soluble and the membrane-bound forms of the enzyme."; EMBO J. 6:3931-3937(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOPO_HUMAN STANDARD; PRT; 603 AA
P09172;
01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J03320; AAA91604.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOPAMINE BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; Nuclease; Endonuclease; Crown gall tumor; Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed.
                    -i- FUNCTION: CONVERSION OF DOPAMINE TO NORADRENALINE.
-i- CATALYTIC ACTIVITY: 3,4-DIHYDROXYPHENETHYLAMINE + ASCORBATE + 0(2)
- NORADRENALINE + DEHYDROASCORBATE + H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-89160241; PubMed-2922261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
-!- COFACTOR: PQQ, COPPER, AND ASCORBATE
                                                                                                                                                                                                                                                 Lamouroux A., Vigny A., Faucon Biguet N., Darmon M.C., Franck R., Henry J.-P., Mallet J.;
                                                                                                                                                                                                                                                                                                                   MEDLINE=88166633; PubMed=3443096
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 17:1089-1102(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Human dopamine beta-hydroxylase gene: two mRNA types having different 3'-terminal regions are produced through alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kobayashi K., Kurosawa Y., Fukita K., Nagatsu T.,
"Human dopamine beta-hydroxylase gene: two mRNA types having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYDROXYLASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                              olyadenylation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 LRIKMAEISLRHG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 MFGSGAGGGRYNYLTAFHIDRDHPHLHVVVNRRELLGHGWLKIS-----RRHPQLNYDA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 ---RASQGSRYEPSITVHL-----WQMAVHTRELLSSGQMPFSQLPAVWQLYPGRKYRA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 LPPDQIHELARSWVQETGTYDESQPDEERQQELTTHIIVSFPAGTSQVAAYAASREWAAE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 VPP-----GRLWIQRPGIYE----DEEGRTWVT--VVVRF-----NPSRREWA-- 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 ADSSFWEIA-DHG 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C22666; C22666.
S11839; S11839.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B22666; B22666.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DBH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.6%;
26.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       603 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
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                                                                                                                                                                                                                                   insights
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                                                         VID2_AGRRH
                                                                         RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- PATHWAY: CATECHOLAMINE BIOSYNTHESIS.
-!- SUBGUNIT: HOMOTETRAMER.
-!- SUBCELLULAR LOCATION: EXISTS BOTH IN A SOLUBLE FORM (IN CHROMAFFIN GRANULES) AND AS MEMBRANE BOUND (THE MEMBRANE BOUND FORM IS ANCHORED BY AN UNCLEAVED SIGNAL PEPTIDE).
-!- INDUCTION: ACTIVITY IS ENHANCED BY MERVE GROWTH FACTOR (IN SUPERIOR CERVICAL GANGLIA & ADREMAL MEDULLA). TRANS-SYNAPTIC STHULLATION WITH RESERPINE, ACETYLCHOLINE AND GLUCOCORTICOIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its
VID2_AGRRH STANDARD;
P13462;
01-Jan-1990 (Rel. 13, Created)
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PIR; S06283; S06283.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00084; CU2_MONOOXYGENASE_1; 1.
PROSITE; PS00085; CU2_MONOOXYGENASE_2; 1.
Catecholamine biosynthesis; Oxidoreductase; Monooxygenase; Copper;
Vitamin C; PQQ; Glycoprotein; Membrane; Signal; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000323; Cu2_monooxygnse.
InterPro; IPR000945; DB_monoxygnse.
Pfam; PF01082; Cu2_monooxygen; 1.
PRINTS; PR00767; DBMONOXGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                       472 EMCVNY 477
                                                                                                                                                                           117 QLVLTY 122
                                                                                                                                                                                                                   429 -----HFQEI-----RMLKKVVSVHPGDVLITSCTYNTEDR---ELATVGGFGILE 471
                                                                                                                                                                                                                                                                                               377 TDKCTQLALPPSGIHIFASQLHTHLTGRKVVTVLVR---DGREWEIVNQDNHYSP---- 428
                                                                                                                                                                                                                                                       63 LWQMAVHTRELLSSGQMPFSQLPAVWQLYPGR-----KYRAADSSFWEIADHGQIDSME 116
                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE COPPER TYPE II, ASCORBATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLYMORPHISM: THERE EXIST TWO FORMS OF DBH: DBH-A AND DBH-B, WHICH DIFFER IN ONE POSITION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MONOOXYGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223360;
                                                                                                                                                                                                                                                                                                                                   SEASVRLGVPPGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWARASQGSRYEPSITVH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S06283; S06283.
                                                                                                                                                                                                                                                                                                                                                                             30;
                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          603 AA;
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67627 MW;
                                                                                                                                                                                                                                                                                                                                                                                              11.6%; Score 79.5; DB 23.8%; Pred. No. 0.74;
                                                                                                                                                                                                                                                                                                                                                                             19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...) (
A-> S (IN DBH-B).
/FTIG-VAR_002196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A -> T (IN REF. 2).
R -> C (IN REF. 2).
39A7A8975111DB5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COPPER (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOPAMINE BETA-MONOOXYGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                            PRT;
                                            436 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                             46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) (POTENTIAL).
) (POTENTIAL).
) (POTENTIAL).
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VID2_AGRT6
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Best Local S
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01-JAN-198B (Rel. 06, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
                                                                                                                    Bacteria; Proteobacteria; Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                        T-DNA BORDER ENDONUCLEASE VIRD2 (EC 3.1.-.-).
Yanoisky M.F., Porter S.G., Young C., Albright L.M., Gordon M.P.,
Nester E.W.;
                                  SEQUENCE FROM N.A.
MEDLINE=87028239; PubMed=3021341;
                                                                                                  NCBI_TaxID=358
                                                                                                                                                                                  Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                 VID2_AGRT6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Organization and characterization of the virCD genes from Agrobacterium rhizogenes.";
MOI. Gen. Genet. 213:229-237(1988).

-I. FUNCTION: TUMOR FORMATION BY A. TUMEFACIENS INVOLVES THE TRANSFER AND INTEGRATION OF A DEFINED SECRUMI (T-DNA) OF TI PLASMID DNA INTO THE PLANT NUCLEAR GENOME. THE VIRD OPERON ENCOMES A SITE-SPECIFIC ENDONUCLEARS THAT CLEAVES AT A UNIQUE SITE WITHIN BOTH 24 BP DIRECT REPEATS FLANKING THE T-DNA.
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20-AUG-2001 (Rel. 40, Last annotation update)
T-DNA BORDER ENDONUCLEASE VIRD2 (EC 3.1.-.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                   163 LRINMAEISLRHG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 MFGSGAGGGSYNYLTAFHIDRDHPHLHVVVNRRELLGHGWLKIS-----RRHPQLNYDA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X12867; CAA31351.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pRiA4b.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 LPPDQIHELARSWVQETGTYDESQPDEERQQELTTHIIVSFPAGTSQAAAYAASREWAAE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 VPP-----GRLWIQRPGIYE----DEEGRTWVT--VVVRF------NPSRREWA-- 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POCGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34; Conservative
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                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.9%; Score 74.5; DB 1; Length 436; 25.6%; Pred. No. 1.7;
                                                                                                                               alpha subdivision; Rhizobiaceae group;
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Poulsen P., Kreiberg J.D.; "Starch branching enzyme cDNA from Solanum tuberosum."; Plant Physiol. 102:1053-1054(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993 (Rel. 26, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (STARCH BRANCHING
                                                                                                                 MEDLINE=94105324; PubMed=8278528;
                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-CV. DIANELLA;
                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                               Solanum tuberosum (Potato)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOLTU
                                                                                                                                                                                                                                                              NCBI_TaxID=4113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jayaswal R.K., Veluthambi K., Gelvin S.B., Slightom J.L.,
"Double-stranded cleavage of T-DNA and generation of single-stranded
T-DNA molecules in Escherichia coli by a viro-encoded
border-specific endonuclease from Agrobacterium tumefaciens.",
J. Bacteriol. 169:5035-5045(1987).

-- FUNCTION: TUMOR FORMATION BY A.TUMEFACIENS INVOLVES THE TRANSFER
AND INTEGRATION OF A DEFINED SEGMENT (T-DNA) OF TI-DASMID DNA
INTO THE PLANT NUCLEAR GENOME. THE VIRD OPERON ENCOMES A SITE-
SPECIFIC ENDONUCLEARS THAT CLEAVES AT A UNIQUE SITE WITHIN BOTH
24 BP DIRECT REPEATS FLANKING THE T-DNA.
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EMBL; M17989; AAA22114.1; -.
PIR; B29826; B29826.
PIR; B2963; B25063.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Nuclease; Endonuclease; Crown gall tumor; Plasmid;
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MEDLINE=88032822; PubMed=2822660;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 SQGS-----RYEPSITVHL-----WQMAVHTRELLSSGQMPFSQLPAVWQL-YPGRKYR 97
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Local Similarity 24.1%;
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Pred. No. 2.7;
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Search completed: November 29, 2001, 04:06:42 Job time: 208 sec
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SEQUENCE
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SEQUENCE OF 279-527 FROM N.A.
STRAIN-CV. DESIREE; TISSUE-Tuber;
MEDLINE-92079917; PubMed-1745241;
KOSSMann J., Visser R.G.F., Mueller-Roeber B., Willmitzer L.,
                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: AMYLOPLAST.
-!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PATHWAY: THIRD STEP IN STARCH BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MO1. Gen. Genet. 230:39-44(1991).
-i- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sonnewald U.; "Cloning and expression analysis of a potato cDNA that encodes branching enzyme: evidence for co-expression of starch biosynthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X69805; CAA49463.1; -. PIR; S18594; S18594.
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                                                                                                                                               667 SFLASGKQIVSSMDDDNKVVVFERGDLVFVFNFHPKNTYEGYKVGCDLPGKYRVALDSDA 726
                                                                                                                                                                                                             620 WIDFP-----REGNNW-----SYDKCRROWNLADSEHLRYK---FMNAFDRAMNSLDEKF 666
                                                                                727 WEFGGHGR 734
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                                                                                                                                                                               73 -LLSSGQMPFS------QLPAVWQLYPGR------KYRAA-DSSF 103
                                                                                                                                                                                                                                            17 WIQRPGIYEDEEGRTWVTVVVRFNPSRREWARA-SQGSRYEPSITVHLWQMAVHTRE--- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gen. Genet. 230:39-44(1991).
                                                                                                                                                                                                                                                                          tch 10.2%; Score 70; DB 1; Length 861; 11 Similarity 24.2%; Pred. NO. 11; 31; Conservative 17; Mismatches 34; Indels
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484 B
553 B
99083 MW;
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BY SIMILARITY.
; F3D519AC7CF1BEF2 CRC64;
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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sp_vertebrate:*
sp_unclassified:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

72.5 10.6 70 10.2 70 10.2	10.9 986 4 10.7 463 2 10.7 464 10 10.7 513 2 10.7 2229 2 10.6 513 2	81 11.8 448 2 79.5 11.6 447 2 79.5 11.6 447 2 79.5 11.5 238 2 76.5 11.2 588 12 76.5 11.1 3742 75.5 11.0 476 2	!
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Q9nxp4 homo sapien	09byf0 homo sarion	OgcayO arabidoneis	074298 penicillium		_		Q98101 infectious		Q82635 infectious	Q99z44 streptococc	Q9uus8 colletotric	Q9w2s6 drosophila	U9K3H3 Streptomyce		Tymantta	1 vman+ ria	025269   vman+ria d	09n859 leishmanta	Q9qpp1 infectious	Q82628 infectious	Q9z514 streptomyce	UZ5142 halocynthia				Oggis7 himan horne	Ogwr38 infactions

AL1GNMENTS

## T next to the TCL1 locus."; Cancer Res. 59:2313-2317(1999). R EMBL; AB025274; BAA82476.1; JOINED. R EMBL; AB025273; BAA82476.1; JOINED. R EMBL; AB025273; BAA82476.1; JOINED. R EMBL; AB018563; BAA876712.1; ... R EMBL; AB018563; BAA76712.1; ... R HSSP; P56278; AIX. R InterPro; IPR002709; TCL1\_MTCP1; 1. SEQUENCE 128 AA; 14945 MW; 6BA2CF22F62CFB4D CRC64; Matches 127; Query Match Best Local S Sugimoto J., Hatakeyama T., Narducci M.G., Russo G., Isobe M.; "Identification of the TCL1/ MTCP1-like 1 (TML1) gene from the region next to the TCL1 locus."; Cancer Res. 59:2313-2317(1999). EMBL; AB025274; BAA82476.1; EMBL; AB025272; BAA82476.1; JOINED. EMBL; AB025273; BAA82476.1; JOINED. EMBL; AB025273; BAA82476.1; JOINED. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-UN-2001 (TrEMBLrel. 17, Last annotation update) TCL1 / MTCP1-LIKE 1. SEQUENCE FROM N.A. MEDLINE=99274532; PubMed=10344735; NCBI\_TaxID=9606; Homo sapiens (Human) Q9UBQ4 Local Similarity 99.2 les 127; Conservative 1 MASEASVRLGVPPGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWARASQGSRYEPSIT 60 PRELIMINARY; 98.8%; Score 677; DB 4; Length 128; 99.2%; Pred. No. 1.3e-62; ative 0; Mismatches 1; Indels PRT; 128 AA. 0; Gaps

121 TYQPERKD 128

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MEDILINE-20056529; PubMed=10588720;
Hallas C., Pekarsky Y., Itoyama T., Varnum J., Bichi R.,
Rothstein J.L., Croce C.M.;
"Genomic analysis of human and mouse TCL1 loc1 reveals a complex of
Lightly clustered genes.";
Proc. Natl. Acad. Sci. U.S.A. 96:14418-14423(1999).
EMBL; AF195491; AAF12804.1; -.
MGD; MGI.1351600; TC11D3.
MGD; MGI.1351600; TC11D3.
SEQUENCE 107 AA; 12224 MW; DDC2AAC489D02DBE CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
T-CELL LEUKEMIA PROTEIN TCL1B3A.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
Enkarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Moriguchi K., Maeda Y., Satou M., Kataoka M., Tanaka N., Yoshida K.; "Analysis of unique variable region of a plant root inducing plasmid, pRi1724, by the construction of its physical map and library."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                     Moriguchi K., Maeda Y., Satou M., Satuti N., Kataoka M., Tanaka N.,
                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-MAFF03-01724;
                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium.
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                                                                      SEQUENCE FROM N.A.
STRAIN=MAFF03-01724;
                                                                                                                                                                                                                                                               NCBI_TaxID=359;
                                                                                                                     "rhe complete nucleotide sequence of a Ri (root inducing) plasmid indicates its chimerical structure between Ti and Sym plasmids."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
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Best Local Similarity 26.8%; Score 81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moriguchi K., Nishida T., Maeda Y., Tanaka N., Yoshida K.; "Genome structure of Ri plasmid (1):Construction of linking library and physical map of pRil724 in Japanese Agrobacterium."; Nucleic Acids Symp. Ser. 39:189-190(1998).
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STRAIN=MAFF03-01724;
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STRAIN-MAFF03-01724;
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Q44461;
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EMBL; AP002086; BAB16287.1; -.
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last ann
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                                                                                                                                                                                                                                                                                  Wang K., Herrera-Estrella A.H., Van Montagu M.M.;
Submitted (JUL-1990) to the EMBL/GenBank/DDBJ databases.
EMBL; M33673; AAA22111.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNKNOWN PROTEIN 2
                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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                                                                                                                                                                                                                                                                                                                                                                                                    Rhizobiaceae; Rhizobium.
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                                 109 MFGSGAGGGRYNYLTAFHIDRDHPHLHVVVNRRELLGHGWLKIS-----RRHPQLNYDA 162
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                                                                                                                                           11 VPP-----GRLWIQRPGIYE----DEEGRTWVT--VVVRF-----NPSRREWA-- 47
                                                                                                                                                                          y match 11.6%; Score 79.5; DB 2; Length 447; Local Similarity 26.3%; Pred. No. 3.4; les 35; Conservative 16. Michael 14.
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 99 ADSSFWEIA-DHG 110
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                                                                      ---RASQGSRYEPSITVHL-----WQMAVHTRELLSSGQMPFSQLPAVWQLYPGRKYRA 98
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                                                                                                                                                                                                                                                                          49649 MW; 9F433A5014B42256 CRC64;
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16; Mismatches 49; Indels 44; Gaps
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163 LRIKMAEISLRHG 175

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Вb
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                                                                      Matches
                                                                                                       Query Match
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                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suzuki K., Ohta N., Hattori Y., Uraji M., Katoh A., Yoshida K.;
"Novel structural difference between nopaline- and octopine- type trbJ
gene:construction of genetic and physical map and sequencing of
trb/tral and rep gene clusters of a new Ti plasmid pTi-SakURA.",
Blochim. Biophys. Acta 1396:1-7(1998).
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MEDLINE=20184752; PubMed=10721727;
SuzUki K., Hattori Y., Uraji M., Ohta N., Iwata K., Murata K., Katoh A., Yoshida K.;
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"Genome structure of pTi-SAKURA (IV): Characteristics of tra region.";
Nucleic Acids Symp. Ser. 39:187-188(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                        Ohta N., Suzuki K., Hattori Y., Uraji M., Katoh A., Yoshida K.; "Genome structure of pTi-SAKURA (III): Characteristics of T-DNA."; Nucleic Acids Symp. Ser. 39:185-186(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh A., Yoshida K.; "Genome structure of pT1-SAKURA(I): Strategy for DNA sequencing of a Japanese cherry-Ti plasmid.";
                                                                                                                                                                                     EMBL; AB016260; BAA87781.1; -.
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MEDLINE=98193120; PubMed=9524202;
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49 LPPDQIHELARSWVQETGTYDESQPDEERQQELTTHIIVSFPAGTSQVAAYAASREWAAE 108
                                  11 VPP-----GRLWIQRPGIYE----DEEGRTWVT--VVVRF------NPSRREWA-- 47
                                                                                   Local Similarity
                                                                                                                                                     447 AA; 49603 MW;
                                                                      Conservative
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                                                                                     11.6%;
26.3%;
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                                                                      16;
                                                                                   Score 79.5; DI Pred. No. 3.4;
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                                                                      Mismatches
                                                                                                   DB 2; Length 447;
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                                      01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
COAT PROFEIN (FRAGMENT).
SUGATCANE Streak mosaic virus.
Viruses; SSRNA positive-Strand viruses, no DNA stage; Potyviridae;
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PRINTS; PR00035; HTHGNYR.
SMART; SM00345; HTH_GNTR; 1.
PROSITE; PS00043; HTH_GNTR,FAMILY; 1.
Complete proteome; DNA-binding; Transcription regulation.
SEQUENCE 238 AA; 26802 MW; 1DAEB7F680EE7F10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
              NCBI_TaxID=53954;
                                                                                                                                                                                  070681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen."; Nature 406:599-594(2000).
                                    Potyvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE004747; AAG06637.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9HYZ1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20437337; PubMed=10984043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PA3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROBABLE TRANSCRIPTIONAL REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9НΥZ1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 MFGSGAGGGRYNYLTAFHIDRDHPHLHVVVNRRELLGHGWLKIS-----RRHPQLNYDA 162
                                                                                                                                                                                                                                                                    88 AMVSEQGRVPATEVLSARQMPASAAVCELLELPALSSVYQIRRARRVDGRLVLYVEH 144
                                                                                                                                                                                                                                                                                                         65 QMA-----VHTRELLSSGQMPFS-----QLPAVWQLYPGRKYRAADSSFWEIADH 109
                                                                                                                                                                                                                                                                                                                                               42 ATTRITLREALIQLESQGLIYREE------RRGWFVSPERLAYNPLVRSHFH 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 LRIKMAEISLRHG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 ADSSFWEIA-DHG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48 ---RASQGSRYEPSITVHL-----WQMAVHTRELLSSGQMPFSQLPAVWQLYPGRKYRA 98
                                                                                                                                                                                                                                                                                                                                                                                   5 ASVRLGVPPGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWARASQGSRYEPSITVHLW 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000524; HTH_GntR.
                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           11.5%;
23.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TO THE GNTR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                           17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 79;
                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                             No.
                                                                                                                                                                                588 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                       46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 238,
                                                                                                                                                                                                                                                                                                                                                                                                                     26; Gaps
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OPTKWB

ACC SUPPLIFIE SEPENCE CONTRACTOR OF SUPPLIFIE SEPENCE 
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                            Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hall J.S., Adams B., Parsons T.J., French R., Lane L., Jensen S.G.; Mol. Phylogenet. Evol. 0:0-0(1998).

EMBL; U75456; AAC16271.1; -. InterPro; IPRO01205; RNA_Pol_P3D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL CHLOROPLAST RF2.
3040 KQSILIH 3046
                                                                                                                                   2988 RAGRALLSSLVPSGYFVGITLFSQRPR-----GRKAEPIYSKIDQKAYE--DHFNAEEC 3039
                                                                                                                                                                                                                                                                         2934 GRLLDDYPHSHSVKSIERGVDVVTSVL--SVDRRQWVRHSTLKTYDPFV----WSRMAYA 2987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Turmel M., Otis C., Lemieux C.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF137379; AAD54848.1; -.
InterPro; IPR003593; AAA.
InterPro; IPR003593; AAA_subfam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99398694; PubMed-10468594;
Turmel M., Otis C., Lemieux C.;
"The complete chloroplast DNA sequence of the green alga Nephroselmis olivacea: Insights into the architecture of ancestral chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9TKW8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9TKW8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 588 AA; 66335 MW; 3876EEF59189EA32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001592; Poty_coat.
Pfam; PF00680; RNA_dep_RNA_pol; 1.
Pfam; PF00767; Poty_coat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Hall J.S., Adams F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chloroplast.
SEQUENCE 3742 AA; 436432 MW; 1F45143EDBC89275 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae; Chlorodendrales; Chlorodendraceae; Nephroselmis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nephroselmis olivacea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=31312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00004; AAA; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 96:10248-10253(1999)
                                                                     116 EQLVLTY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.2%;
Local Similarity 32.8%;
nes 19; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 YERQAGSHWTVGINKFNCGWDELARRFDHNWKFIDADGSRYDSSLTPLLFNCVLHIRE 68
                                                                                                                                                                                                    71 ---RELLSS------GQMPFSQLPAVWQLYPGRK----YRAADSSFWEIADHGQIDSM 115
                                                                                                                                                                                                                                                                                                                                       14 GRLWIQRP---GIYEDEEGRTWVTVVVRFNPSRREWARASQGSRYEPSITVHLWQMAVHT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 YEDEEGRTWVTVVVRFNPSRREWARA-----SQGSRYEPSITVHLWQMAVHTRE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 11.1%; Score 76; DB Local Similarity 29.1%; Pred. No. 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  œ
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                                                                                                                                                                                                                                                                                                                                                                                                                12; Mismatches 46; Indels 32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 76.5; DB 12; Length 588; Pred. No. 9.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3742 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 8; Length 3742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.
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Qy
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                                                                                                                                                                    Q9ULF0
                                                                                                                                                                                     RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00672; DUF5; 1.
Pfam; PF02518; HATPase_C; 1.
Pfam; PF00512; signal; 1.
PRINTS; PR00344; BCTRLSENSOR.
SMART; SM00387; HAMP; 1.
SMART; SM00388; HisKA; 1.
SMART; SM00388; HisKA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C-125 / JCM 9153;
MEDLINE-0512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9KDN8;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
TWO-COMPONENT SENSOR HISTIDINE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9KDN8
                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                Q9ULFO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     halodurans and genomic sequence comparison with Bacillus subtilis.";
Nucleic Acids Res. 28:4317-4331(2000).
-!- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                  KIAA1270 PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP001511; BAB04892.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=86665
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                  Eukaryota; Metazoa;
                                Homo sapiens (Human)
                                                KIAA1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome; Kinase; Phosphorylation; Sensory transduction;
                                                                                                                                                                                                                                                                    118 LVLTYOPERK 127
                                                                                                                                                                                                                                                                                                     174 A---LSLLPAIWLKHYLROPLILLGNRLEQIADRNWKEPFKWEGDEDFQKLSNQFERMRQ 230
                                                                                                                                                                                                                                                                                                                                                                      115 QSRGRYELSYNGATIFYVVTKFNSFGREGYLISYMWDTYRDSMVNRLWERLLYIL-LLSS 173
                                                                                                                                                                                                                                    231 NLVRYDQSQK 240
                                                                                                                                                                                                                                                                                                                                                                                                     19 ORPGIYE-DEEGRTWVTVVVRFNPSRRE-WARASQGSRYEPSITVHLWQMAVHTRELLSS 76
                                                                                                                                                                                                                                                                                                                                    77 GOMPFSQLPAVWQ------LYPGRKYRAADSSF-----WEIAD-----HGQIDSMEQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000410; Bctr
IPR000658; DUF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR003594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         476 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                       11.0%; Score 75.5; DB 2; Length 476; 27.7%; Pred. No. 9.4; ative 16; Mismatches 53; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55661 MW; 0621E01F73E0A319 CRC64;
                  Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bctrl_sensor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HATPase_c
                  Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                476 AA.
                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                           53; Indels 25; Gaps
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                        Stover C.K., Pham X. Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RRA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
rer opportunistic pathogen.";
RA mature 406:959-964(2000).

Br InterPro; IPR001117; Cu-oxidase.
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR001117; Cu-oxidase.
RI InterPro; IPR001117; Cu-oxidase.
RI InterPro; PS00079; MULTICOPPER_OXIDASE1; 1.
PROSITE; PS00079; MULTICOPPER_OXIDASE2; 1.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nagase T., Ishikawa K., Kikuno R., Hirosawa M., Nomura N., Ohara O., "Prediction of the coding sequences of unidentified human genes. XV. The complete sequences of 100 new cDNA clones from brain which code
SEQUENCE
                                                                                                                                                                                                                                                                                              MEDLINE=20437337; PubMed=10984043;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROBABLE METALLO-OXIDOREDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29НХМ7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 986 AA; 107427 MW; E6FDD207907AA831 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00980; TRNASYNTHALA.

PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002106; AA_tRNA_ligase_II.
InterPro; IPR002318; tRNA-synt_2c.
Pfam; PF01411; tRNA-synt_2c; 1.
             Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270 -GLERLVAVLQ 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 DSMEQLVLTYQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 PCTEIH-YDLA-----GGVGAPQLVELWNLVFMQHNREADGSLQPLPQRHVDTGM- 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 GVPPGRLWIQ-----RPGIYEDEEGR-TWVTV-----VVRFNPSRREWARASQGSRYE 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSITVHLWQMAVHTRELLSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEI----ADHGQI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIPEERLWISYFDGDPKAGLDPDLETRDIWLSLGVPASRVLSFGPQENFWEMGDTGP-CG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AB033096; BAA86584.1; -.
463 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
51448 MW; 44222B5DFF9EBCB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 75;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 463 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
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GN DI DI AC
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Q9L8Q3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GLUCURONOSYL TRANSFERASE-LIKE PROTEIN.
                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H., Miyajima N., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome 5. IX.
Sequence features of the regions of 1,011,550 bp covered by seventeen Pl and TAC clones."
DNA Res. 6,183-195(1999).
EMBL: AB017060; BAB10792.1; -.
PUTATIVE ACYL-COA DEHYDROGENASE. PDTORFO.
                                                                                                Q9L8Q3
                                                                                                                   Q9L8Q3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002213; UDP Pfam; PF00201; UDPGT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=COLUMBIA; Pubmed=10470850; MEDLINE=99397451; Pubmed=10470850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9FI99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9FI99;
                                                                                                                                                                                                                                                      118 LYLTYQPERK 127
                                                                                                                                                                                                                  409 AVIRLMVESK 418
                                                                                                                                                                                                                                                                                             356 NGWN---STLESICEG-VPMICLPCKWDQFVNARF---ISEVWRVGIHLEGRIERREIER 408
                                                                                                                                                                                                                                                                                                                                                                          303 LWVVRPG---SVHGRDWIESLPSGFMESLDGKGKIVRWAPQLDVLAHRATGG----FLTH 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 FKTQDAGSYWY---HPHLMSSEQL 145
                                                                                                                                                                                                                                                                                                                                 62 HLWQMAVHTRELLSSGQMPFSQLPAVWQLYPGRKYRAADSSFWEIADH--GQID--SMEQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Watch 10.7%; Score 73; DB 2; Length 463; Local Similarity 24.3%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                16 LWIQRPGIYEDEEGRTWVT--------VVVRFNPSRREWARASQGSRYEPSITV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 RAKQGEWLRVRFTNRLDEPTTIH-WH---GIRLPIEMDGVPYISQPPV---QPGESFIYQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 NPSRREWARASQGSRYEPSITVHLWQMAVHTRELLSSGQMPFSQLPAVWQLYPGR----K 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 LAGLAVVGLGAGGARLWLARPQVAQEYDYELIAAPLDLEIVPGFSSPALAYGGQCPGVEL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 YRAADS-SEWEIADHGQIDSMEQL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MASEASVRLGVPPGRLWIQRPGI-----YEDEEGRTWVTVV-------VRF 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                       31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR002213; UDPGT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464 AA; 52360 MW;
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                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   522E2121F643896D CRC64;
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                                                                                                                 513 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 464;
                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     49; Indels 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
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Q9EWP5
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Best Local
   Pfam; PF00668; Pfam; PF00550;
                                  InterPro; IPR001242; DUF4.
InterPro; IPR003880; Phosphopant_attach.
Pfam; PF00501; AMP-binding; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTARITYE NON-RIBOSOMAL PEPTIDE SYNTHASE.
SC4C2.17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: IPR001552; Acyl-CoA_dh.
Pfam; PF00441; Acyl-CoA_dh; 1.
PR0SITE; PS00072; ACYL_COA_DH_1; UNKNOWN_1.
PR0SITE; PS00073; ACYL_COA_DH_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lewis T.A., Cortese M.S., Sebat J.L., Green T.L., Crawford R.L.;
"Identification of a Region of the Pseudomonas stutzeri strain KC
Chromosome Containing Genes for the Biosynthesis of pyridine-2,6-
bis(thiocarboxylic acid), the Agent of Carbon Tetrachloride
Dechlorination Produced by this Organism.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                          STRAIN=A3(2);
Cerdeno A.M., Parkhill J., Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9EWP5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9EWP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas stutzeri (Pseudomonas perfectomarina)
                                                                                                                                                    "A set of ordered cosmids and a detailed genetic and physical map for
                                                                                                                                                                       Kinashi H., Hopwood D.A.
                                                                                                                                                                                       Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
                                                                                                                                                                                                         MEDLINE-97000351; PubMed-8843436;
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                               Brown S.P.,
                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                      InterPro;
                                                                                                                                                                                                                                                                            Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 LGQLPPRWQLDPSGRLSRLAGTPEANDMIDFSLPNEVQMLVST 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 FSQLPAVWQLYP-GRKYRAADS-SFWEIADHGQIDSMEQLVLT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 FGPRTSRWSRSGKAGRLRVHCHHPQRATCARRNRRQVFVSCHLRHLLHHPHKRRRARGVP 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 FNPSRREWARASQGSR----YEPS-----ITVHLWQMAVHTRELLSSGQMP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                    8 Mb Streptomyces coelicolor A3(2) chromosome.",
. Microbiol. 21:77-96(1996).
L; AL450432; CAC17499.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25;
                                                                                  IPR000873; AMP-bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      513 AA; 57432 MW; 4F6D6E16F30D5C34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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pp-binding;
                  Condensation; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 73; DB
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2229 AA
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19: `
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В
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                                                                Matches
                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  069839;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE IRON-SULFUR BINDING OXIDOREDUCTASE.
                                                                                                                                                                                                                       HSSP; P08980; 1RFS.
Interpro; IPR000205; NAD_binding.
Interpro; IPR001281; Rieske.
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRALN-A3(2);
Parkhill J. Barrell B.G., Rajandream M.A.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphopantetheine.
SEQUENCE 2229 AA; 239295 MW; 66EB782247C326CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50075; ACP_DOMAIN; 3.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
                                                                                                                                                                                                                                                                            the 8 Mb Streptomyces coelicolor A3(2) chromosome.", Mol. Microbiol. 21:77-96(1996).
EMBL; AL023517; CAA18985.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harris D., Taylor K.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             069839
                                                                                                                                                SEQUENCE
                                                                                                                                                                PROSITE; PS00199; RIESKE_1; 1
PROSITE; PS00200; RIESKE_2; U
                                                                                                                                                                                                PRINTS; PR00162; RIESKE
                                                                                                                                                                                                              Pfam; PF00355; Rieske; 1.
                                                                                                                                                                                                                                                                                                                                             Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                Redenbach M.,
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinomycetales; Streptomycineae; Streptomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                              "A set of ordered cosmids and a detailed genetic and physical map for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            934 DGERWYRSGDLARYRPDGVLEFLGRADH 961
436 LPPGEGAVVRAGGGRLAVYRDEEGALHAVSPRCTHLGCLVDFNAAERAWECPCHGSRF 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          878 SVPYGVPLRNMRARVVDGRGRDCPDLVPGELWIGGPGVANGYRGDPGRT----AERFVDH 933
                                11 VPPGRLWIQRPG-----IYEDEEGR-----TWVTVVVRFNPSRREWARASQGSRY 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 SRREWARASQGSRYEPSITVHLWQMAVH 69
                                                                Local Similarity
tes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                513 AA;
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                              Kieser H.M., Denapaite D., Eichner A., Cullum J.,
                                                                                                                                                54931 MW; 06F0987279C9F4AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.78;
28.48;
                                                                                10.6%;
                                                                7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6;
                                                                                                                                                                   UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 73;
Pred. No. :
                                                                            Score 72.5; DB 2; Length 513; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             513 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 2229;
                                                                19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29;
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces.
                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Job time: 222 sec

